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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 33.3149 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218  
Sequence: 1 ALSQPAGHDEPGSGWAA.....GLQNNLSPKYKGPVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1795	80.9	431	4	US-09-912-935-36
2	1066.5	48.1	499	4	US-09-912-935-31
3	1066.5	48.1	529	4	US-09-912-935-28
4	1066.5	48.1	529	4	US-09-912-935-40
5	1055	47.6	449	4	US-09-912-935-34
6	1047.5	47.2	425	4	US-09-912-935-35
7	1044	47.1	530	4	US-09-912-935-38
8	948	42.7	392	4	US-09-764-325A-23
9	948	42.7	392	4	US-09-764-325A-25
10	948	42.7	392	4	US-09-912-935-23
11	948	42.7	392	4	US-09-912-935-25
12	115.5	5.2	1568	3	US-09-181-706-2
13	115.5	5.2	1568	3	US-09-458-791-2
14	115.5	5.2	1568	3	US-09-459-066-2
15	115.5	5.2	1568	4	US-09-459-065-2
16	97	4.4	712	4	US-09-543-681A-6132
17	93.5	4.2	1977	4	US-09-976-594-757
18	93.5	4.2	1977	4	US-09-919-039-367
19	93	4.2	1085	1	US-08-431-080-28
20	93	4.2	1085	2	US-08-938-534-28
21	93	4.2	1085	3	US-09-345-294-28
22	92.5	4.2	1220	1	US-08-158-232-43
23	92.5	4.2	1220	2	US-08-611-928-43
24	92.5	4.2	1220	3	US-09-173-891-43
25	89.5	4.0	424	6	5169835-6
26	89.5	4.0	446	4	US-09-252-991A-31114
27	89	4.0	517	4	US-09-248-796A-14652

ALIGNMENTS

RESULT 1

US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match 80.9%; Score 1795; DB 4; Length 431;  
Best Local Similarity 94.2%; Pred. No. 1.7e-168;  
Matches 343; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	55	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTRQ	114
Db	1	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTRQ	60
Qy	115	ASRVVLSFDPFPYGHPLRQITATGGTFMGDVIHRMLTATQYVAPLMANFNPYSDNST	174
Db	61	ASRVVLSFDPFPYGHPLRQITATGGTFMGDVIHRMLTATQYVAPLMANFNPYSDNST	120
Qy	175	VVYFDNGTVFVQNDHVYVQMGEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	234
Db	121	VVYFDNGTVFVQNDHVYVQMGEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	180
Qy	235	VKTGLSDFAMFLNPSDPVPSRRRSIFHYHRIELDPKSVTMSAVEFTPLTCLQHRSD	294
Db	181	VKTGLSDFAMFLNPSDPVPSRRRSIFHYHRIELDPKSVTMSAVEFTPLTCLQHRSD	240
Qy	295	ACMSDDITFNCSCWCHVLCQRCSSGFDYRQEW-MDYGCAQAEGRMCEDFQD-----ED	346
Db	241	ACMSDDITFNCSCWCHVLCQRCSSGFDYRQEWMDGTGCAQAEAG-----QDVRLPGHRT	294
Qy	347	HDSASPDTSFSPYDGLTITTTSSSLFIDSLATTTEDDTKLNYPAGGDLQNNLSPKTKGTPVH	406
Db	295	TTSASPDTSFSPYDGLTITTTSSSLFIDSLATTTEDDTKLNYPAGGDLQNNLSPKTKGTPVH	354
Qy	407	LGTI	410



Db 215 TVRYEDNGTALVQWHDVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQISSTNH 274  
Qy 234 PVKTGLSDAFMLNPSDPVPSRRSIEYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 293  
Db 275 PVKGLSDAFVVRHRIQIPNVRRTIYEHYRVELQMSKITNISAVENFTPLTCLQFNR 334  
Qy 294 DACMSSDLTFNCWCHVLQRCSSGFDPRYQWMDYGCQAEGRCMCEDFQDEHDHSDSPD 353  
Db 335 GPCVSSQIGFNCWCSKLRQSSGFDPRHQWDSGCPPEESKEKMCENTEPEVTSRTTT 394  
Qy 354 T--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNPYAGGDLQ--NNLSPKTKGTPVHL 407  
Db 395 TVGATTTQFRVLTTTTRRAVTSQFPTSLPTEDDTKIALHLKONGASTDDSAAEKKGTLHA 454  
Qy 408 GTI 410  
Db 455 GLI 457

## RESULT 5

US-09-912-935-34

; Sequence 34, Application US/09912935

; Patent No. 6673904

; GENERAL INFORMATION:

; APPLICANT: Nishikawa, Mitsuho et al.

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483

; CURRENT APPLICATION NUMBER: US/09/912,935

; CURRENT FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: PCT/US00/35260

; PRIOR FILING DATE: 2000-12-23

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 34

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-935-34

Query Match 47.6%; Score 1055; DB 4; Length 449;  
Best Local Similarity 57.2%; Pred. No. 2e-95;  
Matches 202; Conservative 59; Mismatches 86; Indels 6; Gaps 3;

Qy 55 LAMDTLPDNRTRVVED--NHSYVVSRLYGPSPHSELVAVAEANRSQVKIHTILSNTHR 113  
Db 95 LLLDDQDNNTQIEDTTHNYISRIYGPSSASRDLWNIDQMEKDKVKIHGILSNTHR 154  
Qy 114 QASRVLSFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNS 173  
Db 155 QAARVNLISFDPFPYGHPLREITVATGGFIYGEVVRHMLTATQYIAPLMAFNFDPSVRS 214  
Qy 174 TVVYFDNGTVVQWHDVHLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 233  
Db 215 TVRYEDNGTALVQWHDVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQISSTNH 274  
Qy 234 PVKTGLSDAFMLNPSDPVPSRRSIEYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 293  
Db 275 PVKGLSDAFVVRHRIQIPNVRRTIYEHYRVELQMSKITNISAVENFTPLTCLQFNR 334  
Qy 294 DACMSSDLTFNCWCHVLQRCSSGFDPRYQWMDYGCQAEGRCMCEDFQDEHDHSDSPD 353  
Db 335 GPCVSSQIGFNCWCSKLRQSSGFDPRHQWDSGCPPEESKEKMCENTEPEVTSRTTT 394  
Qy 354 T--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNPYAGGDLQ--NNLSPKTKGTPVHL 407  
Db 395 TIGATTTQFRVLTTTTRRAVTSQFPTSLPTEDDTKIALHLKONGASTDDSAAEK 447

## RESULT 6

US-09-912-935-35

; Sequence 35, Application US/09912935

; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuho et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-35

Query Match 47.2%; Score 1047.5; DB 4; Length 425;

Best Local Similarity 56.9%; Pred. No. 1e-94;

Matches 203; Conservative 55; Mismatches 88; Indels 11; Gaps 4;

Qy 61 PDNRTVVVDNHSYVVSRLYGPSPHSELVAVAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 1 PRVRPRVRTD--HNYIISRIYGPSSASRDLWNIDQMEKDKVKIHGILSNTHRQAAVN 59  
Qy 121 SFDPPFYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYF 180  
Db 60 SFDPPFYGHPLREITVATGGFIYGEVVRHMLTATQYIAPLMAFNFDPSVSRNSTV 119  
Qy 181 GTVFWQWHDVHLQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHVPK 240  
Db 120 GTALVQWHDVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQISSTNHP 179  
Qy 241 DAFMLNPSDPVPSRRSIEYHRIELDPKSVTSMASAVEFTPLTCLQHRSCDCM 300  
Db 180 DAFVVRHRIQIPNVRRTIYEHYRVELQMSKITNISAVENFTPLTCLQFNR 239  
Qy 301 LTFNCWCHVLQRCSSGFDPRYQWMDYGCQAEGRCMCEDFQDEHDHSDSPDT 354  
Db 240 IGFNCWCSKLRQSSGFDPRHQWDSGCPPEESKEKMCENTEPEVTELEPPQPERQ 299  
Qy 355 SFSYDGLTTTSSLFIDSFTTDBDTKLNYPAGGDLQ--NNLSPKTKGTPVHLGTI 410  
Db 300 SGSLPPEDAVT---SQFPTSLPTEDDTKIALHLKONGASTDDSAAEKKGTLHAG 353

## RESULT 7

US-09-912-935-38

; Sequence 38, Application US/09912935

; Patent No. 6673904

; GENERAL INFORMATION:

; APPLICANT: Nishikawa, Mitsuho et al.

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483

; CURRENT APPLICATION NUMBER: US/09/912,935

; CURRENT FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: PCT/US00/35260

; PRIOR FILING DATE: 2000-12-23

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 38

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Mouse

US-09-912-935-38

Query Match 47.1%; Score 1044; DB 4; Length 530;

Best Local Similarity 51.3%; Pred. No. 3.2e-94;

Matches 203; Conservative 67; Mismatches 112; Indels 14; Gaps 6;

Qy 27 WNRRAESP GHVSEPDRTQUSQ----DLGGGTGLAMDTLPDNRTRVED--NHSYVVSRLY 81

Db 65 WKRV--DPPRAVDNTRASMGQASPEKGFDTLLDDQDNNTOIEDTDHNYISRYG 122  
Qy 82 PSBHSRLWVDVAEANKRSQVKIHTLSNTHROASRVVLSDFDPFPGYHPLRQIATGGF 141  
Db 123 PADSASRLWNIDQMEKDKVKGILSNTHROAARNVLSDFDPFPGYHPLNEVTATGGF 182  
Qy 142 IFMGDVIHRLMTATQYVAPLANFNPVGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGS 201  
Db 183 IYTGVEVHRMUTATQYIAPLANFNPVGYSDNSTVYFDNGTVFVQWDHVLQDNYNLS 242  
Qy 202 FTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESSRSIF 261  
Db 243 FTFOATLLMDGRILIFGYKEIPVLTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIY 302  
Qy 262 EYHRIELDPKVTMSAVFETPLTCLQHRSCDCAKMSDLTFNCSGCHVLRQCSGDFRY 321  
Db 303 EYHRELQMSKITNISAVEMTPLTCLQFNGCGPCVSSQIGFNCSSWCKLQRCSSGDFRH 362  
Qy 322 ROEMWDYCAQAEAG--RMCEDFQDEHDSASPDTSFSPYDGLTTS---SSLFIDSL 375  
Db 363 RQDWVDSGCPREVOSKEKMCSEKTEPGETSQITTSHTTMOFRVLTITRRRAVTSQMTSL 422  
Qy 376 TTEDDTKLNYPAGSDGLQ--NNLSPKTKGTPVHLGTI 410  
Db 423 PTEDDTKIALHLKDSGASTDSDAAEKKGGTLHAGLI 458

## RESULT 8

US-09-764-325A-23

; Sequence 23, Application US/09764325A

; Patent No. 6667391

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Drmanac, Radoje T.

; APPLICANT: Tang, Y. T.

; APPLICANT: Chao, Cheng-Chi

; APPLICANT: Mize, Nancy K.

; APPLICANT: Childs, John

; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

; FILE REFERENCE: Growth Factor-Like Polypeptides and Polynucleotides

; CURRENT APPLICATION NUMBER: US/09/764,325A

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 09/547,358

; PRIOR FILING DATE: 2000-04-11

; PRIOR FILING DATE: 2000-04-07

; PRIOR FILING DATE: 2000-04-07

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 23

; LENGTH: 392

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-764-325A-23

## Query Match

Best Local Similarity 42.7%; Score 948; DB 4; Length 392;

Matches 184; Conservative 51; Mismatches 77; Indels 6; Gaps 3;

Qy 99 RSQVKIHTLSNTHROASRVVLSDFDPFPGYHPLRQIATGGFIFMGDVIHRLMTATQYV 158  
Db 3 KDKVKIHGILSNTHROAARNVLSDFDPFPGYHPLRQIATGGFIFMGDVIHRLMTATQYI 62  
Qy 159 APLMANFNPVGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOALHHDGRIVPAY 218  
Db 63 APLMANFNPVGYSDNSTVYFDNGTVFVQWDHVLQDNYNLSGFTFOALHHDGRIVPAY 122  
Qy 219 KEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESSRSIFEVHRIELDPKVTMSA 278  
Db 123 KEIPVLTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEVHRELQMSKITNISA 278  
Qy 219 KEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESSRSIFEVHRIELDPKVTMSA 278  
Db 123 KEIPVLTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEVHRELQMSKITNISA 182

Qy 279 VEFTPLPTCLQHRSCDCAKMSDLTFNCSGCHVLRQCSGDFRYQEMDYGCAQAEAGRM 338  
Db 183 VEMTPLPTCLQFNRGCPVSSQIGFNCSSWCKLQRCSSGDFRHRQDWDVSGCPESKEKM 242  
Qy 339 CEDQDEHDSASPD--SFSPYDGLTTS---SSLFIDSLTTEDDTKLNYPAGSDGLQ 393  
Db 243 CENTPEVETSSRTTTTIGATTQFRVLTITRRRAVTSQPTSLPTEDDTKIALHLKDNAS 302  
Qy 394 --NNLSPKTKGTPVHLGTI 410  
Db 303 TDDSAAEKKGGTLHAGLI 320

RESULT 9  
US-09-764-325A-25  
; Sequence 25, Application US/09764325A  
; Patent No. 6667391  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Mize, Nancy K.  
; APPLICANT: Childs, John  
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell  
; FILE REFERENCE: Growth Factor-Like Polypeptides and Polynucleotides  
; CURRENT APPLICATION NUMBER: US/09/764,325A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/547,358  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 09/545,714  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-325A-25

## Query Match 42.7%; Score 948; DB 4; Length 392;

Best Local Similarity 57.9%; Pred. No. 6e-85;

Matches 184; Conservative 51; Mismatches 77; Indels 6; Gaps 3;

Qy 99 RSQVKIHTLSNTHROASRVVLSDFDPFPGYHPLRQIATGGFIFMGDVIHRLMTATQYV 158  
Db 3 KDKVKIHGILSNTHROAARNVLSDFDPFPGYHPLRQIATGGFIFMGDVIHRLMTATQYI 62  
Qy 159 APLMANFNPVGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOALHHDGRIVPAY 218  
Db 63 APLMANFNPVGYSDNSTVYFDNGTVFVQWDHVLQDNYNLSGFTFOALHHDGRIVPAY 122  
Qy 219 KEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESSRSIFEVHRIELDPKVTMSA 278  
Db 123 KEIPVLTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEVHRELQMSKITNISA 182  
Qy 279 VEFTPLPTCLQHRSCDCAKMSDLTFNCSGCHVLRQCSGDFRYQEMDYGCAQAEAGRM 338  
Db 183 VEMTPLPTCLQFNRGCPVSSQIGFNCSSWCKLQRCSSGDFRHRQDWDVSGCPESKEKM 242  
Qy 339 CEDQDEHDSASPD--SFSPYDGLTTS---SSLFIDSLTTEDDTKLNYPAGSDGLQ 393  
Db 243 CENTPEVETSSRTTTTIGATTQFRVLTITRRRAVTSQPTSLPTEDDTKIALHLKDNAS 302  
Qy 394 --NNLSPKTKGTPVHLGTI 410  
Db 303 TDDSAAEKKGGTLHAGLI 320



Matches	184;	Conservative	51;	Mismatches	77;	Indels	6;	Gaps	3
QY	99	RSQVKIHTILSNTHQASRVVL	SFDPFFYGHPLRQIT	ATGGFIFMGDV	VIHRMLTATQYV	158			
Db	3	KDKVKIHGILSNTHQAA	RVLNSFDPFFYGHFLREIT	VATGGFYTGEV	VHRLMTATQYI	62			
QY	159	APLMAINFPGYSNSTV	VVDNGTFTVQWDHYVLQGW	EDKGSFTFOAAL	HHGRIVPAY	218			
Db	63	APLMAINFDPVSNS	TVRYFDNGTALTALVQWDHYV	HLQDNYNLGSGFT	FOATLLMDGRIIFGY	122			
QY	219	KEIPMSVPEISSOH	PKTGLSDAFMLNPS	PDVPESRRSIP	EYHRIELDP	SKVTSMA	278		
Db	123	KEIPVLVTQLS	STNHPKVGLSDAFV	VVHRIQI	PNVRRRII	EYHRLVQLMSKIT	182		
QY	279	VEFTPLPTCLQHR	SCDACMSSDLTFNCS	WCHVLQRCSS	GFDRYRQEWMDY	GCQAQEA	338		
Db	183	VEMTPLPTCLQFN	RCGPCVSSQIGFNC	SWCSKLQRCSS	GFDRHRQD	VWDVSGCP	242		
QY	339	CEDFQEDHDS	ASPD--SFS	PYDGLTTS---	SSLF	FDLSLTED	TKLNPYAGG	393	
Db	243	CENTEPEVTS	SRRTTTTIGATT	QFRVLTTT	RRRAVTSQ	FTSLPTED	DTKIALHLK	302	
QY	394	--NNLS	PKTKGTPVHLGTI	410					
Db	303	TDDSA	AEKKGGLHAGLI	320					
RESULT 12									
US-09-181-706-2									
; Sequence 2, Application US/09181706									
; Patent No. 6130068									
; GENERAL INFORMATION:									
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,									
; APPLICANT: Robert F. DuBoise, Richard S. Johnson									
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN									
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES									
; NUMBER OF SEQUENCES: 10									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Janis C. Henry									
; STREET: 51 University St.									
; CITY: Seattle									
; STATE: WA									
; COUNTRY: US									
; ZIP: 98101									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: Patent In Release #1.0, Version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/09/181,706									
; FILING DATE: October 28, 1998									
; CLASSIFICATION:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 08/958,598 (converted to a									
; APPLICATION NUMBER: Provisional, see below)									
; FILING DATE: October 28, 1997									
; CLASSIFICATION:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: --to be assigned-- (USN 08/958,598									
; APPLICATION NUMBER: conversion to Provisional application)									
; FILING DATE: October 26, 1998									
; CLASSIFICATION:									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Henry, Janis C									
; REGISTRATION NUMBER: 34,347									
; REFERENCE/DOCKET NUMBER: 2631-A									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (206)470-4189									
; TELEFAX: (206)233-0644									
; INFORMATION FOR SEQ ID NO: 2:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 1568 amino acids									

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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-181-706-2

Query Match          5.2%; Score 115.5; DB 3; Length 1568;
Best Local Similarity 20.6%; Pred. No. 0.074;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

Qy 22 GTVGGWNRARRSPGHVSEPDRT-----QLSQDLGGGTLAMDTLDPNTRRVVVDNHNHYVVS 77
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292
Qy 78 RLYGSPSPHRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 122
Db 293 LLLSSSLVEALDVWAGVFAAAGGQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352
Qy 123 -----DPPFYGHPLRQITATGGTFMGDVHRLMTATQYVAPLMAFNPGYSDNSTVY 177
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391
Qy 178 FDNGTVFVQWDHYVLOGWEDKGSFTFOALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
Db 392 LGTG-----FYKLVPDP-----VKNIYIY-----LTAGKEVRRIRVANCNKHS 422
Qy 233 HPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPFSKVTSMASAVEFTPLPTCLOHRS 292
Db 423 TPV-----FYKLVPDP-----VKNIYIY-----LTAGKEVRRIRVANCNKHS 460
Qy 293 CDACMSDLTFNCWCHVLCSSGFDRYRQF-----WMDYCAQAEAGRMCEDFQ-----D 344
Db 461 CSECLTA-TDPHCGWCHSLQRCFTQGDVCHSENLENWLDI-----SSGAKKCPKIQIRSS 515
Qy 345 EDHDSASPDTSFSP 358
Db 516 KEKTTVTWVGFSFSP 529

RESULT 13
US-09-458-791-2
; Sequence 2, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/458,791
; FILING DATE: 10-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644

;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match          5.2%; Score 115.5; DB 3; Length 1568;
Best Local Similarity 20.6%; Pred. No. 0.074;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

Qy 22 GTVGGWNRARRSPGHVSEPDRT-----QLSQDLGGGTLAMDTLDPNTRRVVVDNHNHYVVS 77
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292
Qy 78 RLYGSPSPHRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 122
Db 293 LLLSSSLVEALDVWAGVFAAAGGQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352
Qy 123 -----DPPFYGHPLRQITATGGTFMGDVHRLMTATQYVAPLMAFNPGYSDNSTVY 177
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391
Qy 178 FDNGTVFVQWDHYVLOGWEDKGSFTFOALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
Db 392 LGTG-----FYKLVPDP-----VKNIYIY-----LTAGKEVRRIRVANCNKHS 422
Qy 233 HPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPFSKVTSMASAVEFTPLPTCLOHRS 292
Db 423 TPV-----FYKLVPDP-----VKNIYIY-----LTAGKEVRRIRVANCNKHS 460
Qy 293 CDACMSDLTFNCWCHVLCSSGFDRYRQF-----WMDYCAQAEAGRMCEDFQ-----D 344
Db 461 CSECLTA-TDPHCGWCHSLQRCFTQGDVCHSENLENWLDI-----SSGAKKCPKIQIRSS 515
Qy 345 EDHDSASPDTSFSP 358
Db 516 KEKTTVTWVGFSFSP 529

RESULT 14
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 5.28163 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344  
Perfect score: 370  
Sequence: 1 YHRIELPSKVTSMASVEFT.....CHVLQRCSSGFDRYRQEWMD 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	97.0	431	4	US-09-912-935-36
2	264	71.4	530	4	US-09-912-935-38
3	263	71.1	392	4	US-09-764-325A-23
4	263	71.1	392	4	US-09-764-325A-25
5	263	71.1	392	4	US-09-912-935-23
6	263	71.1	392	4	US-09-912-935-25
7	263	71.1	425	4	US-09-912-935-35
8	263	71.1	449	4	US-09-912-935-34
9	263	71.1	499	4	US-09-912-935-31
10	263	71.1	529	4	US-09-912-935-28
11	263	71.1	529	4	US-09-912-935-40
12	101	27.3	1568	3	US-09-181-706-2
13	101	27.3	1568	3	US-09-458-791-2
14	101	27.3	1568	3	US-09-459-086-2
15	101	27.3	1568	4	US-09-459-065-2
16	63.5	17.2	846	2	US-07-728-215-33
17	63.5	17.2	846	3	US-08-938-085A-33
18	63.5	17.2	846	4	US-10-072-844-33
19	63.5	17.2	846	4	US-10-072-838-33
20	63.5	17.2	846	4	US-10-072-841A-33
21	63.5	17.2	846	4	US-10-219-631-33
22	63	17.0	1404	4	US-09-345-473E-24
23	62.5	16.9	871	3	US-09-245-041-19
24	62.5	16.9	871	4	US-09-358-055B-19
25	62.5	16.9	871	4	US-09-893-238-19
26	62.5	16.9	1198	3	US-09-245-041-131
27	62.5	16.9	1198	3	US-09-794-236-3

28	62.5	16.9	1198	4	US-09-358-055B-132	Sequence 132, App
29	62.5	16.9	1350	3	US-09-245-041-17	Sequence 17, Appl
30	62.5	16.9	1350	4	US-09-358-055B-17	Sequence 17, Appl
31	62.5	16.9	1350	4	US-09-893-238-17	Sequence 17, Appl
32	62.5	16.9	1429	3	US-09-245-041-130	Sequence 130, App
33	62.5	16.9	1429	4	US-09-358-055B-131	Sequence 131, App
34	62.5	16.9	2787	3	US-09-245-041-15	Sequence 15, Appl
35	62.5	16.9	2787	4	US-09-358-055B-15	Sequence 15, Appl
36	62.5	16.9	2787	4	US-09-893-238-15	Sequence 15, Appl
37	61	16.5	138	4	US-09-898-659-30	Sequence 30, Appl
38	60.5	16.4	121	4	US-09-270-767-38436	Sequence 38436, A
39	60.5	16.4	121	4	US-09-270-767-53653	Sequence 53653, A
40	60	16.2	704	4	US-09-370-838-191	Sequence 191, App
41	60	16.2	704	4	US-09-854-133-191	Sequence 1708, Ap
42	59.5	16.1	59	4	US-09-513-999C-6708	Sequence 17517, A
43	59.5	16.1	363	4	US-09-252-991A-17517	Sequence 16, Appl
44	59.5	16.1	939	4	US-09-854-845-16	Sequence 14, Appl
45	59.5	16.1	954	4	US-09-854-845-14	

ALIGNMENTS

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match 97.0%; Score 359; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.5e-36;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	YHRIELPSKVTSMASVEFTPLPTCLQHRSCDACMSDLTFNCMSCHVLQRCSSGFDRYR	60
Db	209	YHRIELPSKVTSMASVEFTPLPTCLQHRSCDACMSDLTFNCMSCHVLQRCSSGFDRYR	268
Qy	61	QEW 63	
Db	269	QEW 271	

RESULT 2  
US-09-912-935-38  
; Sequence 38, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38



FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912.935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 25  
LENGTH: 392  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-25

Query Match 71.1%; Score 263; DB 4; Length 392;  
Best Local Similarity 67.7%; Pred. No. 1.1e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60  
Db 167 YHVELQMSKITNISAVEMTLPCTCLOFNRCPCVSSQIGFNCWSCSKLQRCSSGFDHR 226  
Qy 61 QEWMD 65  
Db 227 QDWVD 231

RESULT 7  
US-09-912-935-35  
Sequence 35, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912.935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 425  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-35

Query Match 71.1%; Score 263; DB 4; Length 425;  
Best Local Similarity 67.7%; Pred. No. 1.3e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60  
Db 202 YHVELQMSKITNISAVEMTLPCTCLOFNRCPCVSSQIGFNCWSCSKLQRCSSGFDHR 261  
Qy 61 QEWMD 65  
Db 262 QDWVD 266

RESULT 8  
US-09-912-935-34  
Sequence 34, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912.935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-34

Query Match 71.1%; Score 263; DB 4; Length 449;  
Best Local Similarity 67.7%; Pred. No. 1.3e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60  
Db 304 YHVELQMSKITNISAVEMTLPCTCLOFNRCPCVSSQIGFNCWSCSKLQRCSSGFDHR 363  
Qy 61 QEWMD 65  
Db 364 QDWVD 368

RESULT 9  
US-09-912-935-31  
Sequence 31, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912.935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 499  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-912-935-31

Query Match 71.1%; Score 263; DB 4; Length 499;  
Best Local Similarity 67.7%; Pred. No. 1.5e-24;  
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60  
Db 274 YHVELQMSKITNISAVEMTLPCTCLOFNRCPCVSSQIGFNCWSCSKLQRCSSGFDHR 333  
Qy 61 QEWMD 65  
Db 334 QDWVD 338

RESULT 10  
US-09-912-935-28  
Sequence 28, Application US/09912935  
Patent No. 6673904  
GENERAL INFORMATION:  
APPLICANT: Nishikawa, Mitsuo et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 32066/37483  
CURRENT APPLICATION NUMBER: US/09/912.935  
CURRENT FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: PCT/US00/35260  
PRIOR FILING DATE: 2000-12-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 529  
TYPE: PRT





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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match 27.3%; Score 101; DB 3; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCCTFQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

RESULT 14
US-09-459-066-2
; Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-066-2

Query Match 27.3%; Score 101; DB 3; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCCTFQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

US-09-459-065-2
; Sequence 2, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,065
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-065-2

Query Match 27.3%; Score 101; DB 4; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCCTFQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2

Query Match 27.3%; Score 101; DB 3; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCCTFQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

RESULT 15
US-09-459-065-2
; Sequence 2, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,065
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-065-2

Query Match 27.3%; Score 101; DB 4; Length 1568;
Best Local Similarity 29.7%; Pred. No. 0.00079;
Matches 22; Conservative 15; Mismatches 27; Indels 10; Gaps 3;

Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55
Db 426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCCTFQ 484
Qy 56 FDRYRQE-----WMD 65
Db 485 GDCVHSENLENWLD 498

Search completed: January 28, 2005, 22:14:14
Job time : 6.53163 secs
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Qy 1 YHRIELDPK-----VTSMASAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSG 55

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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:52:02 ; Search time 130.231 Seconds  
(without alignments)  
1129.372 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218

Sequence: 1 ALSFPQAGHDEFGSGWAA.....GLQNNLSPTKGTFTVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2218	100.0	500	5	Abb90749 Human Tum
2	2218	100.0	500	6	Abu54456 Human tum
3	2218	100.0	500	7	Adi21063 Novel hum
4	2218	100.0	500	8	Adh13230 Human mal
5	2218	100.0	527	7	Adi21554 Novel hum
6	2218	100.0	527	7	Adi21553 Novel hum
7	2218	100.0	1002	5	Abb90723 Human Tum
8	2218	100.0	1002	6	Abu54430 Human tum
9	2134	96.2	488	7	Adi21064 Novel hum
10	1924	86.7	400	3	Aab43131 Human ORF
11	1799.5	81.1	500	5	Abb90783 Mouse Tum
12	1799.5	81.1	500	5	Abb90729 Mouse Tum
13	1799.5	81.1	500	6	Abu54436 Mouse tum
14	1799.5	81.1	500	6	Abu54490 Mouse tum
15	1795	80.9	431	4	Aab85400 Tumour en
16	1795	80.9	431	6	Abo01434 Human tum
17	1215	54.8	240	7	Adb65558 Human pro
18	1066.5	48.1	486	4	Aam39067 Human pol
19	1066.5	48.1	499	4	Aab85396 Stem cell
20	1066.5	48.1	499	6	Abo01430 Human ste
21	1066.5	48.1	529	4	Aab31211 Amino aci
22	1066.5	48.1	529	4	Aab85394 Stem cell
23	1066.5	48.1	529	4	Aau29259 Human PRO
24	1066.5	48.1	529	4	Aam39068 Human pol
25	1066.5	48.1	529	5	Abb90734 Human Tum

#### ALIGNMENTS

RESULT 1  
ABB90749

ID ABB90749 standard; protein; 500 AA.

XX AC ABB90749;

XX DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
normal endothelial marker; pan-endothelial marker; immunostimulant;  
antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
psoriasis.

XX OS Homo sapiens.

XX FN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US024031.

XX PR 02-AUG-2000; 2000US-0222599P.

XX PR 11-AUG-2000; 2000US-0224360P.

XX PR 11-APR-2001; 2001US-0282850P.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX DR WPI; 2002-291856/33.

XX DR N-PSDB; ABL92103.

XX FT An isolated molecule comprising an antibody variable region which  
specifically binds to an extracellular domain of a tumor endothelial  
marker (TEM) protein, useful for inhibiting tumor growth.

XX PS Claim 1; Page 206-207; 31pp; English.

XX CC The invention relates to an isolated molecule comprising an antibody  
variable region which specifically binds to an extracellular domain of a  
tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
proteins have cytostatic, immunostimulant and antiangiogenic activity.  
They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
bearing a vascularised tumour, polycystic kidney disease, diabetic

Abb90726 Human Tum  
Abp53349 Human tra  
Abg69157 Human ste  
Abg69161 Human pro  
Abu58635 Human PRO  
Abu88183 Novel hum  
Abu84498 Human sec  
Abu66372 Human sec  
Abu65762 Human sec  
Abu99702 Human sec  
Abu82941 Human PRO  
Abu90062 Novel hum  
Abu68311 Human sec  
Abu96364 Novel hum  
Abu92795 Human sec  
Abo08872 Human sec  
Abo02924 Human sec  
Abo75078 Human sec  
Abr94840 Human sec  
Abo25182 Novel hum

26 1066.5 48.1 529 5 ABB90726  
27 1066.5 48.1 529 5 ABP53349  
28 1066.5 48.1 529 5 ABG69157  
29 1066.5 48.1 529 5 ABG69161  
30 1066.5 48.1 529 5 ABUS8635  
31 1066.5 48.1 529 6 ABUS88183  
32 1066.5 48.1 529 6 ABUS84498  
33 1066.5 48.1 529 6 ABR66372  
34 1066.5 48.1 529 6 ABR65762  
35 1066.5 48.1 529 6 ABU99702  
36 1066.5 48.1 529 6 ABU82941  
37 1066.5 48.1 529 6 ABU90062  
38 1066.5 48.1 529 6 ABR68311  
39 1066.5 48.1 529 6 ABU96364  
40 1066.5 48.1 529 6 ABU92795  
41 1066.5 48.1 529 6 ABO08872  
42 1066.5 48.1 529 6 ABO02924  
43 1066.5 48.1 529 6 ABR75078  
44 1066.5 48.1 529 6 ABR94840  
45 1066.5 48.1 529 6 ABO25182

CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
 CC are disclosed, as are marker oligonucleotide sequences: tumour  
 CC endothelial markers (TEM) ABL91936-ABL92041 and ABL92143-ABL92191; normal  
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
 CC (PEM) ABL91903-ABL91995  
 XX  
 SQ Sequence 500 AA;

Query Match 100.0%; Score 2218; DB 5; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDQLGGGTAMDTL 60  
 DB 18 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDQLGGGTAMDTL 77  
 QY 61 PDNRTRVVEONHSHYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVL 120  
 DB 78 PDNRTRVVEONHSHYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVL 137  
 QY 121 SFDPFFYGHPLRQITTIATGGIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 180  
 DB 138 SFDPFFYGHPLRQITTIATGGIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 197  
 QY 181 GTVFVQWHDVYLQGWEDKSGFTFQAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 240  
 DB 198 GTVFVQWHDVYLQGWEDKSGFTFQAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 257  
 QY 241 DAFMILNPSDPVPESRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSSD 300  
 DB 258 DAFMILNPSDPVPESRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSSD 317  
 QY 301 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
 DB 318 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
 QY 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410  
 DB 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427

RESULT 2  
 ABUS4456  
 ID ABUS4456 standard; protein; 500 AA.

AC ABUS4456;

XX  
 XX  
 DT 12-MAR-2003 (first entry)

XX Human tumour endothelial marker TEM 17.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
 KW Tumour endothelial marker; normal endothelial marker; PEM;  
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
 KW neovascularization; immune response; cytostatic; antidiabetic;  
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX Homo sapiens.

XX OS

XX WO200283874-A2.

XX PD 24-OCT-2002.

XX 10-APR-2002; 2002WO-0080253.

XX 11-APR-2001; 2001US-0282850P.

XX 06-FEB-2002; 2002US-0354262P.

XX (UTYO ) UNIV JOHNS HOPKINS.

XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

XX  
 DR  
 DR

XX WPI: 2003-093016/08.

XX N-PSDB; ABX72028.

XX New purified human transmembrane protein, designated as tumor endothelial  
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
 PT psoriasis.

XX Disclosure; Page 221-222; 374pp; English.

XX The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. The present  
 CC sequence represents a human TEM or NEM protein of the invention  
 SQ Sequence 500 AA;

Query Match 100.0%; Score 2218; DB 6; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDQLGGGTAMDTL 60  
 DB 18 ALSPPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSDQLGGGTAMDTL 77

QY 61 PDNRTRVVEONHSHYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVL 120

DB 78 PDNRTRVVEONHSHYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVL 137

QY 121 SFDPFFYGHPLRQITTIATGGIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 180

DB 138 SFDPFFYGHPLRQITTIATGGIFMGDVIHRMLTATQVAPLMANFNPGYSDNSTVVFYFDN 197

QY 181 GTVFVQWHDVYLQGWEDKSGFTFQAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 240

DB 198 GTVFVQWHDVYLQGWEDKSGFTFQAALHHDGRIVFAKPEIPMSVPEISSQHPVKTGLS 257

QY 241 DAFMILNPSDPVPESRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSSD 300

DB 258 DAFMILNPSDPVPESRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSSD 317

QY 301 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 360

DB 318 LTFNCNCHVLRQCSGFDRIYQWMDYGCQAQAEGRMCEDFQDEHDSASPDTSFSPYD 377

QY 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410

DB 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427

RESULT 3

ADI21063

ID ADI21063 standard; protein; 500 AA.

XX AC ADI21063;

XX 15-APR-2004 (first entry)

XX Novel human protein #38.

XX forensic; nutritional source; damaged tissue; diseased tissue;

KW myeloid cell disorder; lymphoid cell disorder;

KW bone cartilage tissue growth; tendon tissue growth;

KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;

KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX Homo sapiens.  
XX WO2003025148-A2.  
XX 27-MAR-2003.  
XX 19-SEP-2002; 2002WO-US029964.  
XX 19-SEP-2001; 2001US-0323739P.  
XX 13-SEP-2002; 2002US-00323739.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Qa, Wang J;  
XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
XX Haley-Vicente D;  
XX WPI; 2003-354603/33.  
XX N-PSDB; ADI21779.  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
XX lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
XX tissue growth or regeneration, in wound healing, and in tissue repair and  
XX replacement.  
XX Claim 20; SEQ ID NO 314; 156pp; English.  
XX The invention relates to an isolated polynucleotide encoding a  
XX polypeptide with biological activity. The polynucleotides and  
XX polypeptides are useful in diagnostics, forensics, gene mapping,  
XX identification of mutations responsible for genetic disorders and other  
XX traits, to assess biodiversity, as nutritional sources or supplements.  
XX The polynucleotides may also be used as molecular weight markers,  
XX chromosome markers or map related gene positions, or as an antigen to  
XX raise anti-DNA antibodies or elicit immune response. The polypeptides are  
XX useful for raising antibodies, as markers for tissues in which the  
XX corresponding polypeptide is expressed, for re-engineering damaged or  
XX diseased tissues, for treating myeloid or lymphoid cell disorders, in  
XX bone cartilage, tendon, ligament and/or nerve tissue growth or  
XX regeneration, in wound healing, in tissue repair and replacement, in  
XX healing of burns, incisions and ulcers, and in treating cancer. The  
XX present sequence represents the amino acid sequence of a novel human  
XX protein.  
XX Sequence 500 AA;  
Query Match 100.0%; Score 2218; DB 7; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALSPPQAGHDEPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGGTAMDTL 60  
DB 18 ALSPPQAGHDEPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGGTAMDTL 77  
QY 61 PDNRTRVVDNHSYVGRSLXGPSRSHRELWVDVAENRSQVKHTILSNTHRQASRWL 120  
DB 78 PDNRTRVVDNHSYVGRSLXGPSRSHRELWVDVAENRSQVKHTILSNTHRQASRWL 137  
QY 121 SFDPPFPYGHPLRQITTIATGFIIMGDVTHRMLTATQYVAPLMANFPGYSDNSTVYFDN 180  
DB 138 SFDPPFPYGHPLRQITTIATGFIIMGDVTHRMLTATQYVAPLMANFPGYSDNSTVYFDN 197  
QY 181 GTVPVQWDHYVLCQWEDKSGFTFOAALHDGRIVFAYKIPMSVPEISSQHPVKTGLS 240  
DB 198 GTVPVQWDHYVLCQWEDKSGFTFOAALHDGRIVFAYKIPMSVPEISSQHPVKTGLS 257  
QY 241 DAFMILNPSDVPESRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLQRSCDACMSSD 300  
DB 258 DAFMILNPSDVPESRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLQRSCDACMSSD 317  
QY 301 LTFNCSCWHLQRCSSGFDYRQEMWDYGCQAEGRCMCFQDEDDHDSASPTDSFSPYD 360

DB 318 LTFNCSCWHLQRCSSGFDYRQEMWDYGCQAEGRCMCFQDEDDHDSASPTDSFSPYD 377  
QY 361 GDLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTVPVHLGTI 410  
DB 378 GDLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTVPVHLGTI 427  
RESULT 4  
ADHI3230  
ID ADHI3230 standard; protein; 500 AA.  
XX ADHI3230;  
XX 11-MAR-2004 (first entry)  
XX Human malignant neoplasia-related protein SeqID79.  
XX malignant neoplasia; cytostatic; breast cancer; ovarian cancer;  
XX gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;  
XX bladder cancer; non-small cell lung cancer; human.  
XX Homo sapiens.  
XX EP1385034-A2.  
XX 26-NOV-2003.  
XX 09-MAY-2003; 2003EP-00010447.  
XX 21-MAY-2002; 2002EP-00010291.  
XX 13-FEB-2003; 2003EP-00003112.  
XX (FARB ) BAYER AG.  
XX Wirtz R, Munnes M, Kallabis H;  
XX WPI; 2004-073279/08.  
XX N-PSDB; ADHI3207.  
XX Predicting, diagnosing or prognosing malignant neoplasia by detecting at  
XX least two markers, where the markers are genes from one or more  
XX chromosomal regions altered in malignant neoplasia,.  
XX Claim 11; SEQ ID NO 79; 267pp; English.  
XX This invention relates to a novel method for the prediction, diagnosis,  
XX or prognosis of malignant neoplasia by the detection of at least two  
XX markers. The invention may also be useful for the development of  
XX cytostatic compounds through the regulation of the expression of a gene  
XX or activity of a protein associated with malignant neoplasia. The method  
XX is useful for prediction, diagnosis or prognosis of malignant neoplasia  
XX such as breast cancer, ovarian cancer, gastric cancer, colon cancer,  
XX oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell  
XX lung cancer. The polynucleotides and polypeptides defined in the  
XX specification, antisense polynucleotides targeting the polynucleotides,  
XX antibodies targeting either one of the polynucleotides or polypeptides,  
XX and compounds identified by the screening methods are useful for  
XX preventing or treating malignant neoplasia. The disease treated is  
XX preferably breast cancer. The present sequence is that of a human  
XX malignant neoplasia-related protein which may be used in the method of  
XX the invention.  
XX Sequence 500 AA;  
Query Match 100.0%; Score 2218; DB 8; Length 500;  
Best Local Similarity 100.0%; Pred. No. 2.7e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ALSPPQAGHDEPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGGTAMDTL 60  
DB 18 ALSPPQAGHDEPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGGTAMDTL 77

Qy 61 PDNRTRVEDNHSYVSRLYGSPHSGRELWVDVAEANRSQVKIHTILSNTHROASRVWL 120  
 Db |||||||  
 Qy 78 PDNRTRVEDNHSYVSRLYGSPHSGRELWVDVAEANRSQVKIHTILSNTHROASRVWL 137  
 Db |||||||  
 Qy 121 SFDPFFYGHPLRQITTIATGGFIHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 180  
 Db |||||||  
 Qy 138 SFDPFFYGHPLRQITTIATGGFIHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 197  
 Db |||||||  
 Qy 181 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
 Db |||||||  
 Qy 198 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
 Db |||||||  
 Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSQCDACWSSD 300  
 Db |||||||  
 Qy 258 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSQCDACWSSD 317  
 Db |||||||  
 Qy 301 LTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
 Db |||||||  
 Qy 318 LTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
 Db |||||||  
 Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410  
 Db |||||||  
 Qy 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 427  
 Db |||||||

## RESULT 5

ID ADI21554  
 ADI21554 standard; protein; 527 AA.

XX AC ADI21554;

XX DT 15-APR-2004 (first entry)

XX DE Novel human polypeptide #33.

XX KW forensic; nutritional source; damaged tissue; diseased tissue;

XX KW myeloid cell disorder; lymphoid cell disorder;

XX KW bone cartilage tissue growth; tendon tissue growth;

XX KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;

XX KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

XX OS Homo sapiens.

XX PN WO2003025148-A2.

XX PD 27-MAR-2003.

XX PF 19-SEP-2002; 2002WO-US029964.

XX PR 19-SEP-2001; 2001US-0323739P.

XX PR 13-SEP-2002; 2002US-00323739P.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang Yt, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

XX PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;

XX PI Haley-Vicente D;

XX XX WPI; 2003-354603/33.

XX XX N-PSDB; ADI21334.

XX PT New polynucleotides and secreted proteins, useful for treating myeloid or

XX PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve

XX PT tissue growth or regeneration, in wound healing, and in tissue repair and

XX PT replacement.

XX PS Example 3; SEQ ID NO 805; 156pp; English.

XX CC The invention relates to an isolated polynucleotide encoding a

XX CC polypeptide with biological activity. The polynucleotides and

XX CC polypeptides are useful in diagnostics, forensics, gene mapping,

XX CC identification of mutations responsible for genetic disorders and other

XX CC traits, to assess biodiversity, as nutritional sources or supplements.

CC The polynucleotides may also be used as molecular weight markers,  
 CC chromosome markers or map related gene positions, or as an antigen to  
 CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
 CC useful for raising antibodies, as markers for tissues in which the  
 CC corresponding polypeptide is expressed, for re-engineering damaged or  
 CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
 CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
 CC regeneration, in wound healing, in tissue repair and replacement, in  
 CC healing of burns, incisions and ulcers, and in treating cancer. The  
 CC present sequence represents the amino acid sequence of a novel human  
 CC polypeptide.

XX SQ Sequence 527 AA;

Query Match 100.0%; Score 2218; DB 7; Length 527;

Best Local Similarity 100.0%; Pred. No. 3e-211;

Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPQPGAGHDEGPGSGAAAGTVRGNRRARSPGHVSEPDRTQLSQDLGGGTLAMDTL 60

Db |||||||

Qy 45 ALSPQPGAGHDEGPGSGAAAGTVRGNRRARSPGHVSEPDRTQLSQDLGGGTLAMDTL 104

Db |||||||

Qy 61 PDNRTRVEDNHSYVSRLYGSPHSGRELWVDVAEANRSQVKIHTILSNTHROASRVWL 120

Db |||||||

Qy 105 PDNRTRVEDNHSYVSRLYGSPHSGRELWVDVAEANRSQVKIHTILSNTHROASRVWL 164

Db |||||||

Qy 121 SFDPFFYGHPLRQITTIATGGFIHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 180

Db |||||||

Qy 165 SFDPFFYGHPLRQITTIATGGFIHRLMTATQYVAPLMAFNFGYSDNSTVYVFDN 224

Db |||||||

Qy 181 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240

Db |||||||

Qy 225 GTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 284

Db |||||||

Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSQCDACWSSD 300

Db |||||||

Qy 285 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTPLPTCLOHRSQCDACWSSD 344

Db |||||||

Qy 301 LTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360

Db |||||||

Qy 345 LTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 404

Db |||||||

Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 410

Db |||||||

Qy 405 GDLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTI 454

Db |||||||

## RESULT 6

ADI21553

ID ADI21553 standard; protein; 527 AA.

XX AC ADI21553;

XX DT 15-APR-2004 (first entry)

XX DE Novel human polypeptide #32.

XX KW forensic; nutritional source; damaged tissue; diseased tissue;

XX KW myeloid cell disorder; lymphoid cell disorder;

XX KW bone cartilage tissue growth; tendon tissue growth;

XX KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;

XX KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

XX OS Homo sapiens.

XX PN WO2003025148-A2.

XX PD 27-MAR-2003.

XX PF 19-SEP-2002; 2002WO-US029964.

XX PR 19-SEP-2001; 2001US-0323739P.

XX PR 13-SEP-2002; 2002US-00323739P.

XX (HYSE-) HYSEQ INC.  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX WPI; 2003-354603/33.  
DR N-PSDB; ADI21333.  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX  
PS Example 3; SEQ ID NO 804; 156bp; English.  
XX  
CC The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping,  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC polypeptide.  
XX  
SQ Sequence 527 AA;  
  
Query Match 100.0%; Score 2218; DB 7; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGTILAMDTL 60  
Db 45 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGTILAMDTL 104  
  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 105 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 164  
  
Qy 121 SFDPPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 180  
Db 165 SFDPPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 224  
  
Qy 181 GTVFVQWQDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGS 240  
Db 225 GTVFVQWQDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGS 284  
  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLTCLQHRSCDACMSSD 300  
Db 285 DAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLTCLQHRSCDACMSSD 344  
  
Qy 301 LTFNCSWCHVLQRCSSGFDPRVQEMWYGCQAEGRCNCEFDQEDHDSAPDTSFSPYD 360  
Db 345 LTFNCSWCHVLQRCSSGFDPRVQEMWYGCQAEGRCNCEFDQEDHDSAPDTSFSPYD 404  
  
Qy 361 GDLTTTSSSLFDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 405 GDLTTTSSSLFDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 454  
  
RESULT 7  
ABB90723 standard; protein; 1002 AA.  
ID ABB90723  
XX

AC ABB90723;  
XX  
XX 30-MAY-2002 (first entry)  
XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.  
DE  
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
XX psoriasis.  
XX Homo sapiens.  
OS  
XX WO200210217-A2.  
FN  
XX 07-FEB-2002.  
PD  
XX 01-AUG-2001; 2001WO-US024031.  
PF  
XX 02-AUG-2000; 2000US-0222599P.  
PR  
XX 11-AUG-2000; 2000US-0224360P.  
PR  
XX 11-APR-2001; 2001US-0282850P.  
PR  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA  
XX St Croix B, Kinzler KW, Vogelstein B;  
PI  
XX WPI; 2002-291856/33.  
DR  
XX An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX Disclosure; Page 125-128; 331pp; English.  
XX  
CC The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91936-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
SQ Sequence 1002 AA;  
  
Query Match 100.0%; Score 2218; DB 5; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 8e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGTILAMDTL 60  
Db 520 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPDRTQLSQDLGGTILAMDTL 579  
  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 580 PDNTRVVEDNHSYVSRLYGSPSPHRELVDAEANRSQVKIHTILSNTHRQASRVVL 639  
  
Qy 121 SFDPPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 180  
Db 640 SFDPPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNNTVVYFDN 699  
  
Qy 181 GTVFVQWQDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGS 240  
Db 700 GTVFVQWQDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGS 759  
  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLTCLQHRSCDACMSSD 300

Db 760 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPLPTCLOHRSACDACWSSD 819  
Qy 301 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQBAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 820 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQBAEGRMCEDFQDEHDSASPDTSFSPYD 879  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 880 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 929

RESULT 8  
ABU54430  
ID ABU54430 standard; protein; 1002 AA.  
XX  
AC ABU54430;  
XX  
DT 12-MAR-2003 (first entry)  
XX  
DE Human tumour endothelial marker TEM 8.  
XX  
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neoangiogenesis; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipeoriatic.  
XX  
OS Homo sapiens.  
XX  
XX WO200283874-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 10-APR-2002; 2002WO-US008253.  
XX  
XX 11-APR-2001; 2001US-0282850P.  
XX  
XX 06-FEB-2002; 2002US-0354262P.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX  
XX WPI; 2003-093016/08.  
XX  
XX N-FSDB; ABX72003.  
XX  
XX New purified human transmembrane protein, designated as tumor endothelial  
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
XX psoriasis.  
XX  
XX Disclosure; Page 122-124; 374pp; English.  
XX  
XX The present invention relates to a novel method for the isolation of  
XX endothelial cells (ECs), and the identification of genes expressed in  
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal  
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
XX identified in human ECs. The human EC marker proteins and the  
XX polynucleotide sequences encoding them are useful for detecting,  
XX diagnosing or treating tumours as well as polycystic kidney disease,  
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
XX useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
XX inducing an immune response to tumour endothelial cells in a patient, or  
XX for identifying candidate drugs for treating tumours. The present  
XX sequence represents a human TEM or NEM protein of the invention  
XX  
SQ Sequence 1002 AA;

Query Match 100.0%; Score 2218; DB 6; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 8e-211;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSPQPCAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 60  
Db 520 ALSPQPCAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL 579  
Qy 61 PDNRTRVVEDNHYSYVRLYGPSEPHSRRELWVDVAEANRSQVKIHTILSNTHRQASRVL 120  
Db 580 PDNRTRVVEDNHYSYVRLYGPSEPHSRRELWVDVAEANRSQVKIHTILSNTHRQASRVL 639  
Qy 121 SFDPFPYGHPLRQITATGGFIWGDVHRLMTATQYVAPLMANFNPGYSDNSTVYVFDN 180  
Db 640 SFDPFPYGHPLRQITATGGFIWGDVHRLMTATQYVAPLMANFNPGYSDNSTVYVFDN 699  
Qy 181 GTVFVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPRISSQHSPVKTGLS 240  
Db 700 GTVFVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPRISSQHSPVKTGLS 759  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPLPTCLOHRSACDACWSSD 300  
Db 760 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPLPTCLOHRSACDACWSSD 819  
Qy 301 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQBAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 820 LTFNCSWCHVLQRCSSGFDRIYQWMDYGCQAQBAEGRMCEDFQDEHDSASPDTSFSPYD 879  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 880 GDLTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 929

RESULT 9  
ADI21064  
ID ADI21064 standard; protein; 488 AA.  
XX  
AC ADI21064;  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Novel human protein #39.  
XX  
KW forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003025148-A2.  
XX  
XX 27-MAR-2003.  
XX  
XX 19-SEP-2002; 2002WO-US029964.  
XX  
XX 19-SEP-2001; 2001US-0323739P.  
XX  
XX 13-SEP-2002; 2002US-00323739.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
XX Haley-Vicente D;  
XX  
XX WPI; 2003-354603/33.  
XX  
XX N-FSDB; ADI21780.  
XX  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
XX lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
XX tissue growth or regeneration, in wound healing, and in tissue repair and  
XX replacement.  
XX  
XX Claim 20; SEQ ID NO 315; 156pp; English.  
XX  
XX The invention relates to an isolated polynucleotide encoding a



CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping,  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC protein.  
XX  
XX  
SQ Sequence 488 AA;

Query Match 96.2%; Score 2134; DB 7; Length 488;  
Best Local Similarity 97.1%; Pred. NO. 6e-203;  
Matches 398; Conservative 0; Mismatches 0; Indels 12; Gaps 1;  
  
Qy 1 ALSPPGAGHDEGPGSGAAAGTGVGNRRARESPGHVSEPDRTQLSODLGGGTAMDTL 60  
Db 18 ALSPPGAGHDEGPGSGAAAGTGVGNRRARESPGHVSEPDRTQLSODLGGGTAMDTL 77  
  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHSELRWDVAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 78 PDNTRVVEDNHSYVSRLYGSPSPHSELRWDVAEANRSQVKIHTILSNTHRQASRVVL 137  
  
Qy 121 SFDPFFYGHPLRQITATGGIFMGDVTHRMILTATQYVAPLMAFNPGYSDNSTVVPFDN 180  
Db 138 SFDPFFYGHPLRQITATGGIFMGDVTHRMILTATQYVAPLMAFNPGYSDNSTVVPFDN 197  
  
Qy 181 GTVFVQWDHVVYLOGWEDKGSFTFOALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWDHVVYLOGWEDKGSFTFOALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 257  
  
Qy 241 DAFMLNPSDPVPESRRSIFEYHRIELDPKVTSMASVETPTLCTLQHRSCDACMSSD 300  
Db 258 DAFMLNPSDPVPESRRSIFEYHRIELDPKVTSMASVETPTLCTLQHRSCDACMSSD 317  
  
Qy 301 LTFNCSWCHVLQRCSSGPDYRQEMDYGCAQEAEGRCNCFQDEHDHDSASPDTSFSPYD 360  
Db 318 LTFNCSWCHVLQRCSSGPDYRQEMDYGCAQEAEGRCNCFQDEHDHDSASPDTSFSPYD 377  
  
Qy 361 GDLTTSSSLFDSLTTFEDDTKLPYAGDGLQNNLSPTKGTVPVHLGTI 410  
Db 378 GDLTTSSSLFDSLTTFE-----GLQNNLSPTKGTVPVHLGTI 415

RESULT 10  
RAB43131  
ID AAB43131 standard; protein; 400 AA.  
AC AAB43131;  
XX  
XX  
DT 08-FEB-2001 (first entry)  
XX Human ORFX ORF2895 polypeptide sequence SEQ ID NO:5790.  
DE  
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnary; antipariatic; antiparkinsonian; nectropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antihemetic; antithyroid;  
KW antinaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.  
XX  
XX Homo sapiens.  
XX WO2000058473-A2.  
XX  
PD 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US008621.  
XX  
PR 31-MAR-1999; 99US-0127607P.  
PR 02-APR-1999; 99US-0127636P.  
PR 05-APR-1999; 99US-0127728P.  
PR 30-MAR-2000; 2000US-00540763.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
PI WPI; 2000-602362/57.  
XX  
DR N-PSDB; AAC77340.  
XX  
XX Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease.  
XX  
PS Claim 11; Page 4955; 5507pp; English.  
XX  
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;  
CC antipariatic; antiparkinsonian; nectropic; neuroprotective; osteopathic;  
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;  
CC antiviral; antifungal; antineumatic; antichyroid; and antinaemic. The  
CC sequences can be used for determining the presence of or predisposition  
CC to, or preventing or treating pathological conditions associated with an  
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX  
CC proteins in gene therapy vectors. The proteins and nucleic acids may be  
CC used to treat cancers, proliferative disorders, neurodegenerative  
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
CC storage, systemic lupus erythematosus, severe combined immunodeficiency  
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and  
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to  
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive  
XX  
SQ Sequence 400 AA;

Query Match 86.7%; Score 1924; DB 3; Length 400;  
Best Local Similarity 100.0%; Pred. NO. 3.6e-182;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ALSPPGAGHDEGPGSGAAAGTGVGNRRARESPGHVSEPDRTQLSODLGGGTAMDTL 60  
Db 46 ALSPPGAGHDEGPGSGAAAGTGVGNRRARESPGHVSEPDRTQLSODLGGGTAMDTL 105  
  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHSELRWDVAEANRSQVKIHTILSNTHRQASRVVL 120  
Db 106 PDNTRVVEDNHSYVSRLYGSPSPHSELRWDVAEANRSQVKIHTILSNTHRQASRVVL 165  
  
Qy 121 SFDPFFYGHPLRQITATGGIFMGDVTHRMILTATQYVAPLMAFNPGYSDNSTVVPFDN 180  
Db 166 SFDPFFYGHPLRQITATGGIFMGDVTHRMILTATQYVAPLMAFNPGYSDNSTVVPFDN 225  
  
Qy 181 GTVFVQWDHVVYLOGWEDKGSFTFOALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 240  
Db 226 GTVFVQWDHVVYLOGWEDKGSFTFOALHHDGRIVFAVKEIPMSVPEISSQHPVKTGLS 285  
  
Qy 241 DAFMLNPSDPVPESRRSIFEYHRIELDPKVTSMASVETPTLCTLQHRSCDACMSSD 300

```

Db 286 DAFMLNPSDPVPSRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 345
Qy 301 LTFNCSCWCHVLQRCSSGFDYRQEMWDYGCAQEAEGRMCEDFQDEHDSASPD 354
Db 346 LTFNCSCWCHVLQRCSSGFDYRQEMWDYGCAQEAEGRMCEDFQDEHDSASPD 399

RESULT 11
ID ABB90783 standard; protein; 500 AA.
AC ABB90783;
XX
XX 30-MAY-2002 (first entry)
XX
XX Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis.
XX
XX Mus musculus.
XX
XX WO200210217-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US024031.
XX
XX 02-AUG-2000; 2000US-0222599P.
XX
XX 11-AUG-2000; 2000US-0224360P.
XX
XX 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2002-291856/33.
XX
XX N-PSDB; ABL92136.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Disclosure; Page 301-302; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour; polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92073-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences: tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995
XX
XX Sequence 500 AA;

Query Match 81.1%; Score 1799.5; DB 5; Length 500;
Best Local Similarity 80.7%; Pred. No. 1.2e-169;
Matches 331; Conservative 39; Mismatches 33; Indels 1; Gaps 1;

Qy 1 ALSPOPAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSODLGGGTIAMD 60
Db 19 ALSPATPAGHDEGQSAWTAKTROGWRRRPRESPAQLKFGKTLQSLDGLGSLAIDTL 78

61 PDNRTYVEDNHSYYSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHQASRVVL 120
Db 79 PDNRTYVEDNHNYYISRVYGPGEKQSDWDLAVANRSHVKIHRILSSSHRQASRVVL 138
Qy 121 SFDPFFYGHPLRQITTIATGCFIFMGDVIHRLMTATQYVAPLMAFNFGYSDNSTVYFDN 180
Db 139 SFDPFFYGHPLRQITTIATGCFIFMGDMLHRLMTATQYVAPLMAFNFGYSDNSTVYFDN 198
Qy 181 GTVPVQWDHVIYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHHPVKTGLS 240
Db 199 GTVPVQWDHVIYLOQDREDRGSFTFOALHRDGRIVFGYKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300
Db 259 DAFMLNPSPEVPESQRTIFEYHRELDSSKITTTSAAVEFTPLTCLQHQSCDTCVSSN 318
Qy 301 LTFNCSCWCHVLQRCSSGFDYRQEMWDYGCAQEAEGRMCEDFQDEHDSASPDTSFSPYD 360
Db 319 LTFNCSCWCHVLQRCSSGFDYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASPDSSFSFPFN 378
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 GD-STTSSSLFIDSLTTEDDTKLNPYAEGDGLPDHSPKSKGPPVHLGTI 427

RESULT 12
ABB90729
ID ABB90729 standard; protein; 500 AA.
XX
XX AC ABB90729;
XX
XX 30-MAY-2002 (first entry)
XX
XX Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis.
XX
XX Mus musculus.
XX
XX WO200210217-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US024031.
XX
XX 02-AUG-2000; 2000US-0222599P.
XX
XX 11-AUG-2000; 2000US-0224360P.
XX
XX 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2002-291856/33.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Disclosure; Page 146-147; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM

```

CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
XX Sequence 500 AA;

Query Match 81.1%; Score 1799.5; DB 5; Length 500;  
Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
QY 1 ALSPOGAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGWRRPRESPAQVLKPKGTQLSQDLGGGSLAIDTL 78  
QY 61 PDNTRVVEDNHSYVSLYGPSPHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 120  
Db 79 PDNTRVVEDNHSYVSRVYGPGEQSDQLWDLAVANRSHVKIHRILSSHRQASRVVL 138  
QY 121 SFDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMANFNPGYSDNSTVYFDN 180  
Db 139 SFDFPFYGHPLRQITATGGFIFMGDLHRLMTATQYVAPLMANFNPGYSDNSTVYFDN 198  
QY 181 GTVFVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTGILS 240  
Db 199 GTVFVQWDHVLQDREDRGSFTFOALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
QY 241 DAFMLNPSDPVPSRRRSIPEYHRIELDPKVTSMASAVEFTPLPTCLQHSRCDACMSD 300  
Db 259 DAFMLNPSPEVPESQRTIPEYHRVELDSSKITTSAVEFTPLPTCLQHSRCDTCVSSN 318  
QY 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEFDQDHDHDSASPDTSFSPYD 360  
Db 319 LTFNCSWCHVLQRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPDSSFSFPN 378  
QY 361 GDLTTSSSLFIDSITTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSITTEDDTKLNYPABGDGLPDHSSPKSKGPPVHLGTI 427

RESULT 13  
ABUS4436  
ID ABUS4436 standard; protein; 500 AA.  
XX  
XX AC ABUS4436;  
XX  
XX DT 12-MAR-2003 (first entry)  
XX  
XX DE Mouse tumour endothelial marker TEM 7.  
XX  
XX KW Mouse; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neoangiogenesis; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
XX  
XX OS Mus musculus.  
XX  
XX PN WO200283874-A2.  
XX  
XX PD 24-OCT-2002.  
XX  
XX PF 10-APR-2002; 2002WO-US008253.  
XX  
XX PR 11-APR-2001; 2001US-0282850P.  
XX  
XX PR 06-FEB-2002; 2002US-0354262P.  
XX  
XX PA (UWJO ) UNIV JOHNS HOPKINS.  
XX  
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX

DR WPI; 2003-093016/08.  
DR N-PSDB; ABX72008.  
XX  
XX PT New purified human transmembrane protein, designated as tumor endothelial  
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors, or  
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
XX psoriasis.  
XX  
XX PS Disclosure; Page 147-148; 374pp; English.  
XX  
XX CC The present invention relates to a novel method for the isolation of  
XX endothelial cells (ECs), and the identification of genes expressed in  
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal  
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
XX identified in human ECs. The human EC marker proteins and the  
XX polynucleotide sequences encoding them are useful for detecting,  
XX diagnosing or treating tumours as well as polycystic kidney disease,  
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
XX useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
XX inducing an immune response to tumour endothelial cells in a patient, or  
XX for identifying candidate drugs for treating tumours. The present  
XX sequence represents a mouse TEM protein  
XX  
XX Sequence 500 AA;  
Query Match 81.1%; Score 1799.5; DB 6; Length 500;  
Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
QY 1 ALSPOGAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGWRRPRESPAQVLKPKGTQLSQDLGGGSLAIDTL 78  
QY 61 PDNTRVVEDNHSYVSLYGPSPHRELWVDVAENRSQVKIHTILSNTHRQASRVVL 120  
Db 79 PDNTRVVEDNHSYVSRVYGPGEQSDQLWDLAVANRSHVKIHRILSSHRQASRVVL 138  
QY 121 SFDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMANFNPGYSDNSTVYFDN 180  
Db 139 SFDFPFYGHPLRQITATGGFIFMGDLHRLMTATQYVAPLMANFNPGYSDNSTVYFDN 198  
QY 181 GTVFVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTGILS 240  
Db 199 GTVFVQWDHVLQDREDRGSFTFOALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
QY 241 DAFMLNPSDPVPSRRRSIPEYHRIELDPKVTSMASAVEFTPLPTCLQHSRCDACMSD 300  
Db 259 DAFMLNPSPEVPESQRTIPEYHRVELDSSKITTSAVEFTPLPTCLQHSRCDTCVSSN 318  
QY 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEFDQDHDHDSASPDTSFSPYD 360  
Db 319 LTFNCSWCHVLQRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPDSSFSFPN 378  
QY 361 GDLTTSSSLFIDSITTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSITTEDDTKLNYPABGDGLPDHSSPKSKGPPVHLGTI 427  
RESULT 14  
ABUS4490  
ID ABUS4490 standard; protein; 500 AA.  
XX  
XX AC ABUS4490;  
XX  
XX DT 12-MAR-2003 (first entry)  
XX  
XX DE Mouse tumour endothelial marker mTEM 9.  
XX  
XX KW Mouse; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neoangiogenesis; immune response; cytostatic; antidiabetic;  
KW

KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

OS Mus sp.

XX WO200283874-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US008253.

XX 11-APR-2001; 2001US-0282850P.

XX 06-FEB-2002; 2002US-0354262P.

XX (UYVJ) UNIV JOHNS HOPKINS.

XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2003-093016/08.

XX N-PSDB; ABX72061.

XX New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

XX Disclosure; Page 339-340; 374pp; English.

XX The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumor ECs. Tumor endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumors as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a mouse TEM protein

XX Sequence 500 AA;

Query Match 81.1%; Score 1799.5; DB 6; Length 500;  
Best Local Similarity 80.7%; Pred. No. 1.2e-169;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

QY 1 ALSPOFGAGHDEGPGSGWAAGTGVGNRRARESPGHVSEPDRTQLSDLGGLAMDTL 60

DB 19 ALSPATPAGHNEGQDSAWTAKTRQGSRRPRESPAQLKPKTKLSQDLGGSLAIDTL 78

QY 61 PDNTRVVDNHSYVSLYGPSPHRELWVDVAENRSQVKIHTILSNTHROASRVVL 120

DB 79 PDNTRVVDNHSYVSLYGPSPHRELWVDVAENRSQVKIHTILSNTHROASRVVL 138

QY 121 SFDPFFYGHPLRQITATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVWYFDN 180

DB 139 SFDPFFYGHPLRQITATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVWYFDN 198

QY 181 GTVFVQWDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGS 240

DB 199 GTVFVQWDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258

QY 241 DAFMTLNSPDVPSRRRSIPEYHRIELDPKYSMSAVEFTPLTCLOHRSQCDACSSD 300

DB 259 DAFMTLNSPEVPSQRRTIPEYHREVLDSKITTSAVEFTPLTCLOHRSQCDTCVSSN 318

QY 301 LTFNCSWCHVLQRCSSGDFRVRQEMWYGCQAEGRCMEDFQBDHDSASPDTSFSPYD 360

DB 319 LTFNCSWCHVLQRCSSGDFRVRQEWLTYGCAQAEAGTKCEDFQDDSHYSASPDSSFPFN 378

QY 361 GDLTTSSSLFIDSLTTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410

DB 379 GD-STTSSSLFIDSLTTDDTKLNPYAGDGLPDHSSPKSKGPPVHLGTI 427

RESULT 15

XX AAB85400

XX ID AAB85400 standard; protein; 431 AA.

XX AC AAB85400;

XX DT 17-SEP-2001 (first entry)

XX Tumour endothelial marker 7 precursor protein.

XX Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; Alzheimer's disease; nutritional supplement; cytosolic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; tumour endothelial marker 7 precursor protein.

XX OS Homo sapiens.

XX PN WO200153500-A1.

XX PD 26-JUL-2001.

XX PF 23-DEC-2000; 2000WO-US035260.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 07-APR-2000; 2000US-00545714.

XX PR 11-APR-2000; 2000US-00547358.

XX PA (HYSE-) HYSEQ INC.

XX PI Labat I, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;

XX FI Chao C;

XX DR WPI; 2001-451909/48.

XX Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs.

XX Example 4; Page 149-150; 154pp; English.

XX The invention provides novel human stem cell growth factor-like polypeptides and polynucleotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polynucleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may aid patients in need of transplants. They can also be used as nutritional supplements. The present sequence represents a tumour endothelial marker 7 precursor protein, homologous to a stem cell growth factor-like polypeptide

XX Sequence 431 AA;

Query Match 80.9%; Score 1795; DB 4; Length 431;

Best Local Similarity 94.2%; Pred. No. 2.8e-169;

Matches 343; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

QY 55 LAMDTLPDNRTRVVDNHSYVSLYGPSPHRELWVDVAENRSQVKIHTILSNTHRO 114

DB 1 LAMDTLPDNRTRVVDNHSYVSLYGPSPHRELWVDVAENRSQVKIHTILSNTHRO 60

QY 115 ASRVVLSFDPFFYGHPLRQITATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSDNST 174

DB 61 ASRVVLSFDPFFYGHPLRQITATGGIFMGDVIHRMLTATQYVAPLMAFNPGYSDNST 120

QY 175 VVYFDNGTIVFVQWHDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 234

DB 121 VVYFDNGTIVFVQWHDHYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180

QY 235 VKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSCD 294  
Db |||||  
181 VKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRSCD 240  
QY 295 ACMSSDLTFNCSCWCHVLRQCSGFDYRQEW-MDYGCAOEAEGRMCEDFOD-----ED 346  
Db |||||  
241 ACMSSDLTFNCSCWCHVLRQCSGFDYRQEWDTGTWGCQAEAG-----QDVRGLPGNRT 294  
QY 347 HDSASPDTSFSPYDGLTTTSSSLFIDSLLTTEDDTKLNPIYAGDGLQNNLSPKTKGTPVH 406  
Db |||||  
295 TTASASPDTSFSPYDGLTTTSSSLFIDSLLTTEDDTKLNPIYAGDGLQNNLSPKTKGTPVH 354  
QY 407 LGTI 410  
Db ||||  
355 LGTI 358

Search completed: January 28, 2005, 22:05:04  
Job time : 132.231 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:59:20 ; Search time 112.059 Seconds  
(without alignments)  
1321.880 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218

Sequence: 1 ALSPPQAGHDEGPGSGWAA.....GLQNLSPKTKGTPVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2218	100.0	500	10	US-09-918-715-230
2	2218	100.0	500	15	Sequence 230, App
3	2218	100.0	500	17	Sequence 79, Appl
4	2218	100.0	500	17	Sequence 230, App
5	2218	100.0	500	17	Sequence 2, Appli
6	2218	100.0	1002	10	Sequence 179, App
7	2134	96.2	488	17	Sequence 4, Appli
8	2093	94.4	502	14	Sequence 5, Appli
9	1799.5	81.1	500	10	Sequence 192, App
10	1799.5	81.1	500	10	Sequence 192, App
11	1799.5	81.1	500	14	Sequence 297, App
12	1799.5	81.1	500	17	Sequence 6, Appli
13	1799.5	81.1	500	17	Sequence 192, App
					Sequence 237, App

14	1795	80.9	431	10	US-09-912-935-36	Sequence 36, Appl
15	1795	80.9	431	14	US-10-168-365-36	Sequence 36, Appl
16	1215	54.8	240	14	US-10-104-047-3712	Sequence 3712, Ap
17	1066.5	48.1	499	10	US-09-912-935-31	Sequence 31, Appl
18	1066.5	48.1	499	14	US-10-168-365-31	Sequence 31, Appl
19	1066.5	48.1	529	10	US-09-918-715-189	Sequence 189, App
20	1066.5	48.1	529	10	US-09-918-715-200	Sequence 200, App
21	1066.5	48.1	529	10	US-09-912-935-28	Sequence 28, Appl
22	1066.5	48.1	529	10	US-09-912-935-40	Sequence 40, Appl
23	1066.5	48.1	529	13	US-10-052-586-472	Sequence 472, App
24	1066.5	48.1	529	13	US-10-066-500-128	Sequence 128, App
25	1066.5	48.1	529	14	US-10-174-590-472	Sequence 472, App
26	1066.5	48.1	529	14	US-10-176-758-472	Sequence 472, App
27	1066.5	48.1	529	14	US-10-175-737-472	Sequence 472, App
28	1066.5	48.1	529	14	US-10-174-581-472	Sequence 472, App
29	1066.5	48.1	529	14	US-10-176-483-472	Sequence 472, App
30	1066.5	48.1	529	14	US-10-176-749-472	Sequence 472, App
31	1066.5	48.1	529	14	US-10-176-914-472	Sequence 472, App
32	1066.5	48.1	529	14	US-10-176-915-472	Sequence 472, App
33	1066.5	48.1	529	14	US-10-173-706-472	Sequence 472, App
34	1066.5	48.1	529	14	US-10-175-738-472	Sequence 472, App
35	1066.5	48.1	529	14	US-10-175-752-472	Sequence 472, App
36	1066.5	48.1	529	14	US-10-176-482-472	Sequence 472, App
37	1066.5	48.1	529	14	US-10-176-757-472	Sequence 472, App
38	1066.5	48.1	529	14	US-10-176-913-472	Sequence 472, App
39	1066.5	48.1	529	14	US-10-180-552-472	Sequence 472, App
40	1066.5	48.1	529	14	US-10-180-557-472	Sequence 472, App
41	1066.5	48.1	529	14	US-10-173-700-472	Sequence 472, App
42	1066.5	48.1	529	14	US-10-174-572-472	Sequence 472, App
43	1066.5	48.1	529	14	US-10-174-579-472	Sequence 472, App
44	1066.5	48.1	529	14	US-10-174-582-472	Sequence 472, App
45	1066.5	48.1	529	14	US-10-174-588-472	Sequence 472, App

ALIGNMENTS

RESULT 1

US-09-918-715-230  
; Sequence 230, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 230  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-230

Query Match 100.0%; Score 2218; DB 10; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSODLGGGTLMADTL 60  
Db 18 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSODLGGGTLMADTL 77  
Qy 61 PDNTRVVDNHSYVYVRLYQSPHRELWVDVAENRSQVKHTILSNTHRQASRVVL 120

Db 78 PDNRTRVVEDNHSYVSRLYGSPBSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 137  
Qy 121 SFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYFDN 180  
Db 138 SFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYFDN 197  
Qy 181 GTVFVQWDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300  
Db 258 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 317  
Qy 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
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Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
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## RESULT 2

US-10-435-696-79  
; Sequence 79, Application US/10435696  
; Publication No. US20040018525A1  
; GENERAL INFORMATION:  
; APPLICANT: Wirtz, Ralph  
; APPLICANT: Munnes, Marc  
; APPLICANT: Kallabis, Harald  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS  
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA  
; FILE REFERENCE: Lea 36 108  
; CURRENT APPLICATION NUMBER: US/10/435,696  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: EP03003112.4  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: EP02010291.9  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 314  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 79  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-435-696-79

Query Match 100.0%; Score 2218; DB 15; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60  
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77  
Qy 61 PDNRTRVVEDNHSYVSRLYGSPBSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 78 PDNRTRVVEDNHSYVSRLYGSPBSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 137  
Qy 121 SFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYFDN 180  
Db 138 SFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYFDN 197  
Qy 181 GTVFVQWDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300  
Db 258 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 317  
Qy 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 318 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377

Db 318 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 427  
RESULT 3  
US-10-474-794-230  
; Sequence 230, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/308,829  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 230  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-474-794-230

Query Match 100.0%; Score 2218; DB 17; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60  
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77  
Qy 61 PDNRTRVVEDNHSYVSRLYGSPBSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 78 PDNRTRVVEDNHSYVSRLYGSPBSPHRELVDAEANRSQVKIHTILSNTHROASRVVL 137  
Qy 121 SFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYFDN 180  
Db 138 SFDPFPYGHPLRQITATGGFIEMGDVIRHMLTATQYVAPLMAFNFGYSDNSTVYFDN 197  
Qy 181 GTVFVQWDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWDHVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
Qy 241 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300  
Db 258 DAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 317  
Qy 301 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db 318 LTFNCSWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 378 GDLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTI 427

## RESULT 4

US-10-357-819-2  
; Sequence 2, Application US/10357819  
; Publication No. US20040259774A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Edinger, Shlomit R.



; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Li, Li  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Raestelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-538A  
; CURRENT APPLICATION NUMBER: US/10/357,819  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 09/584,411  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 09/783,436  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 10/085,198  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/353,301  
; PRIOR FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: 60/355,099  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: 60/356,424  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/358,239  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/358,608  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/359,367  
; PRIOR FILING DATE: 2002-02-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 2  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-357-819-2

Query Match 100.0%; Score 2218; DB 17; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMDTL 60  
Db 18 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMDTL 77  
  
Qy 61 PDRTRVVDNHSYVSLYGPSPHRELWVDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 78 PDRTRVVDNHSYVSLYGPSPHRELWVDAEANRSQVKIHTILSNTHROASRVVL 137  
  
Qy 121 SFDPFPYGHPLRQITATGGFIHMGDVIHRLMTATQYVAPLMANFPGYSDNSTVYVFDN 180  
Db 138 SFDPFPYGHPLRQITATGGFIHMGDVIHRLMTATQYVAPLMANFPGYSDNSTVYVFDN 197  
  
Qy 191 GTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 198 GTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300  
Db 258 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 317

Qy 301 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAEGRMCEDFQDEHDSASPDTSFSFYD 360  
Db 318 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAEGRMCEDFQDEHDSASPDTSFSFYD 377  
  
Qy 361 GDLTTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSFKTKGTVPVHLGTI 410  
Db 378 GDLTTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSFKTKGTVPVHLGTI 427  
  
RESULT 5  
US-09-918-715-179  
; Sequence 179, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Kenneth Kinzler  
; APPLICANT: Bert Vogelstein  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 179  
; LENGTH: 1002  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-918-715-179

Query Match 100.0%; Score 2218; DB 10; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 4.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMDTL 60  
Db 520 ALSPPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMDTL 579  
  
Qy 61 PDRTRVVDNHSYVSLYGPSPHRELWVDAEANRSQVKIHTILSNTHROASRVVL 120  
Db 580 PDRTRVVDNHSYVSLYGPSPHRELWVDAEANRSQVKIHTILSNTHROASRVVL 639  
  
Qy 121 SFDPFPYGHPLRQITATGGFIHMGDVIHRLMTATQYVAPLMANFPGYSDNSTVYVFDN 180  
Db 640 SFDPFPYGHPLRQITATGGFIHMGDVIHRLMTATQYVAPLMANFPGYSDNSTVYVFDN 699  
  
Qy 181 GTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 700 GTVFVQWHDVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 759  
  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300  
Db 760 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 819  
  
Qy 301 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAEGRMCEDFQDEHDSASPDTSFSFYD 360  
Db 820 LTFNCSCWHLQRCSSGFDYRQWMDYGCQAEGRMCEDFQDEHDSASPDTSFSFYD 879  
  
Qy 361 GDLTTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSFKTKGTVPVHLGTI 410  
Db 880 GDLTTTSSSLFIDSLLTTEDDTKLNYPAGGDLQNNLSFKTKGTVPVHLGTI 929

RESULT 6  
US-10-474-794-179  
; Sequence 179, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:

; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; PRIOR FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 179  
; LENGTH: 1002  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-474-794-179

Query Match 100.0%; Score 2218; DB 17; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 4.5e-203;  
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ALSPOPAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60  
Db |  
520 ALSPOPAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 579  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120  
Db |  
580 PDNTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 639  
Qy 121 SFDPFFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMAFNFGYSDNSTVYVFDN 180  
Db |  
640 SFDPFFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMAFNFGYSDNSTVYVFDN 699  
Qy 181 GTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGSL 240  
Db |  
700 GTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGSL 759  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVETPLPTCLQHRSCDACMSSD 300  
Db |  
760 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVETPLPTCLQHRSCDACMSSD 819  
Qy 301 LTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQEAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db |  
820 LTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQEAEGRMCEDFQDEHDSASPDTSFSPYD 879  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGTPVHLGTI 410  
Db |  
880 GDLTTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGTPVHLGTI 929

RESULT 7  
US-10-357-819-4  
; Sequence 4, Application US/10357819  
; Publication No. US20040259774A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Li, Li  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rastelli, Inca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-538A  
; CURRENT APPLICATION NUMBER: US/10/357,819  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 09/584,411  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 09/783,436  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 10/085,198  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/353,301  
; PRIOR FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: 60/355,099  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: 60/356,424  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 60/358,239  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/358,608  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/359,367  
; PRIOR FILING DATE: 2002-02-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: Curaseq1ist version 0.1  
; SEQ ID NO 4  
; LENGTH: 488  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-357-819-4

Query Match 96.2%; Score 2134; DB 17; Length 488;  
Best Local Similarity 97.1%; Pred. No. 1.7e-195;  
Matches 398; Conservative 0; Mismatches 0; Indels 12; Gaps 1;  
  
Qy 1 ALSPOPAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60  
Db |  
18 ALSPOPAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77  
Qy 61 PDNTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120  
Db |  
78 PDNTRVVEDNHSYVSRLYGSPSPHRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137  
Qy 121 SFDPFFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMAFNFGYSDNSTVYVFDN 180  
Db |  
138 SFDPFFYGHPLRQITATGGFIEMGDVHRMLTATQYVAPLMAFNFGYSDNSTVYVFDN 197  
Qy 181 GTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGSL 240  
Db |  
198 GTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGSL 257  
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVETPLPTCLQHRSCDACMSSD 300  
Db |  
258 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVETPLPTCLQHRSCDACMSSD 317  
Qy 301 LTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQEAEGRMCEDFQDEHDSASPDTSFSPYD 360  
Db |  
318 LTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQEAEGRMCEDFQDEHDSASPDTSFSPYD 377  
Qy 361 GDLTTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGTPVHLGTI 410  
Db |  
378 GDLTTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGTPVHLGTI 415

RESULT 8  
US-10-156-487A-5  
; Sequence 5, Application US/10156487A  
; Publication No. US20030092025A1

```
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match      94.4%; Score 2093; DB 14; Length 502;
Best Local Similarity 95.0%; Pred. No. 1.5e-191;
Matches 397; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 18 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 77
Qy 61 PDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
Db 78 PDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 138 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 197
Qy 181 GTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAKEIPMSVPEISSQHPVKTGLS 240
Db 198 GTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAKEIPMSVPEISSQHPVKTGLS 257
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300
Db 258 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 317
Qy 301 LTFNCSCWCHVLRQCSGFDYRQEW-MDYGCAQAEAGMCEDFQD-----EHDGASP 352
Db 318 LTFNCSCWCHVLRQCSGFDYRQEWDMGTGMCQAEG-----QDVRGLPGMRTTTSASP 371
Qy 353 DTSPSPYDGLTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410
Db 372 DTSPSPYDGLTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 429

RESULT 9
US-09-918-715-192
; Sequence 192, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-297

Query Match      81.1%; Score 1799,5; DB 10; Length 500;
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKRTQGSRRRPRESPAQVLPKPKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
Db 79 PDNRTRVVEDNHSYVSRVYGPGEKQSDLMVDLAVANRSHVKIHRILSSSHRQASRVVL 138
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 139 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 198
Qy 181 GTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAKEIPMSVPEISSQHPVKTGLS 240
Db 199 GTVFVQWQDHVYLQDREDGSGFTFOAALHHDGRIVFGVKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300
Db 259 DAFMLNPSPEVPSQRRTIFEYHVELDSSKITTTSAVEFTPLTCLQHQSCDTCVSSN 318
Qy 301 LTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAQAEAGMCEDFQDDEHDSASPDTSFSPYD 360
Db 319 LTFNCSCWCHVLRQCSGFDYRQEWLTYGCAQAEAGTKCEDFQDDSHYSASPDSSFPFN 378
Qy 361 GDLTTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 GD-STTSSSLFIDSLLTDDTKLNPYAGDGLPDHSSPKSKGPPVHLGTI 427
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```
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-192

Query Match      81.1%; Score 1799,5; DB 10; Length 500;
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKRTQGSRRRPRESPAQVLPKPKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
Db 79 PDNRTRVVEDNHSYVSRVYGPGEKQSDLMVDLAVANRSHVKIHRILSSSHRQASRVVL 138
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 139 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 198
Qy 181 GTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAKEIPMSVPEISSQHPVKTGLS 240
Db 199 GTVFVQWQDHVYLQDREDGSGFTFOAALHHDGRIVFGVKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300
Db 259 DAFMLNPSPEVPSQRRTIFEYHVELDSSKITTTSAVEFTPLTCLQHQSCDTCVSSN 318
Qy 301 LTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAQAEAGMCEDFQDDEHDSASPDTSFSPYD 360
Db 319 LTFNCSCWCHVLRQCSGFDYRQEWLTYGCAQAEAGTKCEDFQDDSHYSASPDSSFPFN 378
Qy 361 GDLTTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 GD-STTSSSLFIDSLLTDDTKLNPYAGDGLPDHSSPKSKGPPVHLGTI 427

RESULT 10
US-09-918-715-297
; Sequence 297, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 297
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mouse
US-09-918-715-297

Query Match      81.1%; Score 1799,5; DB 10; Length 500;
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTLMADTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKRTQGSRRRPRESPAQVLPKPKTQLSQDLGGGSLAIDTL 78
Qy 61 PDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
Db 79 PDNRTRVVEDNHSYVSRVYGPGEKQSDLMVDLAVANRSHVKIHRILSSSHRQASRVVL 138
Qy 121 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 180
Db 139 SFDPFPYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYVFDN 198
Qy 181 GTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAKEIPMSVPEISSQHPVKTGLS 240
Db 199 GTVFVQWQDHVYLQDREDGSGFTFOAALHHDGRIVFGVKEIPMAVLDISSAQHPVKAGLS 258
Qy 241 DAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCDACMSSD 300
Db 259 DAFMLNPSPEVPSQRRTIFEYHVELDSSKITTTSAVEFTPLTCLQHQSCDTCVSSN 318
Qy 301 LTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAQAEAGMCEDFQDDEHDSASPDTSFSPYD 360
Db 319 LTFNCSCWCHVLRQCSGFDYRQEWLTYGCAQAEAGTKCEDFQDDSHYSASPDSSFPFN 378
Qy 361 GDLTTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 GD-STTSSSLFIDSLLTDDTKLNPYAGDGLPDHSSPKSKGPPVHLGTI 427
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Db PDNRTRVEDNHNYYVSRVYGEKQSQDLWDLAVANRSHVKIHRILSSHQASRVVL 138  
Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNDSTVVYFDN 180  
Db 139 SFDPFFYGHPLRQITTIATGGFIFMGDMLHRMLTATQYVAPLMAFNPGYSNDSTVAYFDN 198  
Qy 181 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 199 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
Qy 241 DAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDACMSSD 300  
Db 259 DAFMILNPSPEVPESSRRRSIFEYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDTCVSSN 318  
Qy 301 LTFNCSWCHVLQRCSSGDRYQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 360  
Db 319 LTFNCSWCHVLQRCSSGDRYQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 378  
Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSLLTTEDDTKLNPAAGDGLPDHSSSPKSGPPVHLGTI 427

## RESULT 11

US-10-156-487A-6  
; Sequence 6, Application US/10156487A  
; Publication No. US2003092025A1  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Olinier, John  
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A  
; CURRENT APPLICATION NUMBER: US/10/156,487A  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-156-487A-6

Query Match 81.1%; Score 1799.5; DB 14; Length 500;  
Best Local Similarity 80.7%; Pred. No. 2.2e-163;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
Qy 1 ALSPOGAGHDGPGSGWAAKGTVRGNRRARSPGHVSEBPDRTQLSQDLGGGTLMADTLL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGNRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78  
Qy 61 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSHQASRVVL 120  
Db 79 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSHQASRVVL 138  
Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNDSTVVYFDN 180  
Db 139 SFDPFFYGHPLRQITTIATGGFIFMGDMLHRMLTATQYVAPLMAFNPGYSNDSTVAYFDN 198  
Qy 181 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 199 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
Qy 241 DAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDACMSSD 300  
Db 259 DAFMILNPSPEVPESSRRRSIFEYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDTCVSSN 318  
Qy 301 LTFNCSWCHVLQRCSSGDRYQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 360  
Db 319 LTFNCSWCHVLQRCSSGDRYQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 378

Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSLLTTEDDTKLNPAAGDGLPDHSSSPKSGPPVHLGTI 427  
RESULT 12  
US-10-474-794-192  
; Sequence 192, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 192  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-474-794-192

Query Match 81.1%; Score 1799.5; DB 17; Length 500;  
Best Local Similarity 80.7%; Pred. No. 2.2e-163;  
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;  
Qy 1 ALSPOGAGHDGPGSGWAAKGTVRGNRRARSPGHVSEBPDRTQLSQDLGGGTLMADTLL 60  
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGNRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78  
Qy 61 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSHQASRVVL 120  
Db 79 PDNRTRVEDNHNYYVSRVYGEKRSQDLWDLAVANRSHVKIHRILSSHQASRVVL 138  
Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSNDSTVVYFDN 180  
Db 139 SFDPFFYGHPLRQITTIATGGFIFMGDMLHRMLTATQYVAPLMAFNPGYSNDSTVAYFDN 198  
Qy 181 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
Db 199 GTVFVQWDHVYLVQWEDKGSFTFOAALHHDGRIVFAYKEIPMAVLDISSAQHPVKAGLS 258  
Qy 241 DAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDACMSSD 300  
Db 259 DAFMILNPSPEVPESSRRRSIFEYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDTCVSSN 318  
Qy 301 LTFNCSWCHVLQRCSSGDRYQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 360  
Db 319 LTFNCSWCHVLQRCSSGDRYQEWMDYGCQAEGRCMCEDFQDDSHYSASPDSSFSFPFN 378  
Qy 361 GDLTTSSSLFIDSLLTTEDDTKLNPAAGDGLQNNLSPKTKGTPVHLGTI 410  
Db 379 GD-STTSSSLFIDSLLTTEDDTKLNPAAGDGLPDHSSSPKSGPPVHLGTI 427

## RESULT 13

US-10-474-794-297  
; Sequence 297, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS



Db 181 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLQHRSCD 240  
Qy 295 ACMSSDLTFNCSCWCHVLCRCSSGFDRYRQEW-MDYGCAQEAEGRCEDFQD-----ED 346  
Db 241 ACMSSDLTFNCSCWCHVLCRCSSGFDRYRQEWDTMGCAQEAEG-----QDVRGLPGMRT 294  
Qy 347 HDSASPDTSFSPYDGLTTTSSLFIDSLLTTEDDTKLNPNYAGGDLQNNLSPKTKGTPVH 406  
Db 295 TTSASPDTSFSPYDGLTTTSSLFIDSLLTTEDDTKLNPNYAGGDLQNNLSPKTKGTPVH 354  
Qy 407 LGTI 410  
Db 355 LGTI 358

Search completed: January 28, 2005, 22:19:20  
Job time : 113.059 secs



F:21-1161/Product: nidogen #status predicted <MAT>  
E:274-306/Domain: EGF homology <EG1>  
F:560-574/Region: 3-residue repeats (R-P-V)  
F:603-673/Domain: thyroglobulin type I repeat homology <THY1>  
F:686-748/Domain: thyroglobulin type I repeat homology <THY2>  
F:752-819/Domain: thyroglobulin type I repeat homology <THY3>  
F:900-943/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
F:944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
F:987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
F:1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F:1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW5>  
F:1129-1158/Domain: EGF homology <EG2>  
F:107,334,360,484/Binding site: carboxydrate (Asn) #status predicted

Query Match 20.9%; Score 123; DB 1; Length 1161;  
Best Local Similarity 28.0%; Pred. No. 7.7e-05;  
Matches 40; Conservative 18; Mismatches 41; Indels 44; Gaps 5;

Qy 1 LSPDFPPFYGHPLRQITTIATGGFIFM-----GDVHRMLTATQYVAPLMAN----- 45  
Db 47 LSMPIVFVDQKYSVTVHTDGFILNVGADTDGEVL-----LAPFMSDLDTLSG 97

Qy 46 --FNPFGSDNSTVYV-----FDNGTFVFWQDHYVLOGWEDKGSFTFQAA 88  
Db 98 DIFFREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWVKVQSASREDGVITFTQCI 157

Qy 89 LHHQGRIVFA---YKEIPMSVPE 108  
Db 158 VATDGAATFAIFLYPQDGLAVGE 180

RESULT 3  
T30243  
alpha tectorin - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: T30243  
R:Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.  
Hear. Res. 130, 62-74, 1999

A:Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.  
A:Reference number: 220783; MUID:99251817; PMID:10320099  
A:Accession: T30243  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2120 <COU>  
A:Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAC  
A:Note: non-collagenous protein only expressed in the inner ear

Query Match 14.3%; Score 84; DB 2; Length 2120;  
Best Local Similarity 27.1%; Pred. No. 2.3;  
Matches 38; Conservative 14; Mismatches 46; Indels 42; Gaps 8;

Qy 1 LSPDFPPFYGHPLRQITTIATGGFIFMGDVIHR-----MLTATQYVAPL-----MAN----- 45  
Db 51 LSVPFIFRSPRYRTVYNNNGVIGFNSLSVQFTPEAPPLADGRAFPVAPFCGDVANGIRGE 110

Qy 46 -----FNP---GYSDNSTVYFDN-----GTFVFWQDHYVLOGWEDKGSF-----TF 85  
Db 111 IYRESTNPPELLGSSKDIRYKDMASFSASWFIVTWEVQPYG-----GSSTPVNTF 166

Qy 86 QAALHHDC---RIVFAYKEI 102  
Db 167 QAVLITDGVSSFAIFNYQEI 186

RESULT 4  
A60165  
sodium channel protein - fruit fly (Drosophila melanogaster) (fragments)  
C:Species: Drosophila melanogaster  
C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: S04029; A60165  
R:Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.  
Nucleic Acids Res. 15, 8569-8572, 1987

A:Title: Nucleotide sequence of the putative sodium channel gene from Drosophila: the fo  
A:Reference number: S04029; MUID:88040482; PMID:2444928  
A:Accession: S04029  
A:Molecule type: DNA  
A:Residues: 1-362;363-626;627-1321 <SAL>  
A:Cross-references: UNIPROT:Q27930; EMBL:X14394  
R:Salkoff, L.; Butler, A.; Wei, A.; Scavarda, N.; Giffen, K.; Ifune, C.; Goodman, R.; Ma:  
Science 237, 744-749, 1987  
A:Title: Genomic organization and deduced amino acid sequence of a putative sodium chann  
A:Reference number: A60165; MUID:87292090; PMID:2441469  
A:Accession: A60165  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 40-355;363-560,'P',562-626;632-1263 <SA2>  
A:Cross-references: EMBL:X14394  
A:Note: part of this sequence was confirmed by mRNA sequencing  
A:Note: the authors' translation is shown at position 561  
C:Genetics:  
A:Gene: FlyBase:NaCP60E  
A:Cross-references: FlyBase:FBgn0002920  
A:Introns: 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1; 626/3; 751/2; 801/1; 908/1;  
Query Match 14.2%; Score 83.5; DB 2; Length 1321;  
Best Local Similarity 31.1%; Pred. No. 1.5;  
Matches 19; Conservative 12; Mismatches 25; Indels 5; Gaps 2;

Qy 9 GHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMANFNGYSNSTVYFDNGTFVFWQ 68  
Db 1171 GHPLLAITYFT-SFI-----IISYIVINMYITAILENFNOAQHQBEEIGIVEDDLEMPYIR 1235

Qy 69 W 69  
Db 1226 W 1226

RESULT 5  
JC7853  
L-fucose-specific lectin - Aspergillus oryzae  
C:Species: Aspergillus oryzae  
C>Date: 18-Nov-2002 #sequence\_revision 18-Nov-2002 #text\_change 09-Jul-2004  
C:Accession: JC7853; PC7191  
R:Ishida, H.; Moritani, T.; Hata, Y.; Kawato, A.; Suginami, K.; Abe, Y.; Imayasu, S.  
Biosci. Biotechnol. Biochem. 66, 1002-1008, 2002  
A:Title: Molecular cloning and overexpression of fLeA gene encoding a fucose-specific le  
A:Reference number: JC7853; MUID:22087106; PMID:12092808  
A:Accession: JC7853  
A:Molecule type: DNA  
A:Residues: 1-310 <ISH>  
A:Cross-references: UNIPROT:Q8TGE0; DDBJ:AB072379  
A:Experimental source: strain OSI1018  
A:Accession: PC7191  
A:Molecule type: protein  
A:Residues: 132-147;148-177 <IS2>  
C:Comment: This protein, with ferrichrysin-affinity, has hemagglutination activity again  
C:Genetics:  
A:Gene: fLeA  
A:Introns: 12/1; 71/3; 143/1; 177/2

Query Match 13.4%; Score 79; DB 2; Length 310;  
Best Local Similarity 45.2%; Pred. No. 0.78;  
Matches 19; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

Qy 45 NFNPFGSDNSTVYFDN--GTFVFWQDHYVLOGWEDKGSFT 84  
Db 219 NFNPFGSSIIYRIYFVNSDNTIWQVCWDHG--QGYHDKRTIT 258

RESULT 6  
T30197  
alpha tectorin - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T30197



Qy 97 PAYKEIPMSVPE 108  
|| :: | :  
Db 220 FAIRDVAKSIKQ 231

RESULT 10  
C95048



## RESULT 14

JC4553  
heme d1 synthesis protein nirF - Pseudomonas aeruginosa  
C:Species: Pseudomonas aeruginosa  
C:Date: 12-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: JC4553; H83581  
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.  
Gene 167, 87-91, 1995  
A:Title: Sequencing and characterization of the downstream region of the genes encoding Y for biosynthesis of heme d1.  
A:Reference number: JC4552; MUID:96144254; PMID:8566817  
A:Accession: JC4553  
A:Molecule type: DNA  
A:Residues: 1-392 <KAW>  
A:Cross-references: UNIPROT:Q51480; DDBJ:D50473; NID:gl217594; PIDN:BAA09066.1; PID:gl217594  
A:Experimental source: RM31  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bader, G.; Lory, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83581  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-392 <STO>  
A:Cross-references: GB:AE004488; GB:AE004091; NID:g9946372; PIDN:AAG03905.1; GSPDB:GN001488  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: nirF; PA0516  
C:Superfamily: Pseudomonas stutzeri heme d1 synthesis protein nirF

Query Match 11.4%; Score 67; DB 2; Length 392;  
Best Local Similarity 28.2%; Pred. No. 20;  
Matches 22; Conservative 10; Mismatches 30; Indels 16; Gaps 2;  
Qy 37 QYVAPLMAFNPGYSDNSTV-----YFNGTVFV---QWDHVLQGWEDK 80  
Db 134 ELVAEIPATRLPGQDRNSRVGLVDAPGQRFVSLFDSGEIWIADFSQGDTPHLTRFDI 193  
Qy 81 GSFTFOAALHHDGRIVFA 98  
Db 194 GKQPYDALISPDGRYYNA 211

## RESULT 15

B82510  
transporter, NadC family VCA0025 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: B82510  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chaudhuri, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, J.; R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: B82510  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-462 <HEI>  
A:Cross-references: UNIPROT:Q9KNE0; GB:AE004346; GB:AE003853; NID:g9657401; PIDN:AAF9593  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VCA0025  
A:Map position: 2  
C:Superfamily: probable transporter MJ0672

Query Match 11.4%; Score 67; DB 2; Length 462;  
Best Local Similarity 23.9%; Pred. No. 24;  
Matches 17; Conservative 14; Mismatches 26; Indels 14; Gaps 2;

Qy 23 IFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGS 82  
Db 58 LMLTEALH--VTVTAILVPVMAVFFGIFETQAAALNNFANSIIFLF-----LGG 103  
Qy 83 FTFOAALHHDG 93  
Db 104 FALAANVHHQG 114

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Job time : 9.47923 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:56:43 ; Search time 40.6279 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLRLREARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/6C.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	81.2	431	4	US-09-912-935-36
2	1295	48.1	499	4	US-09-912-935-31
3	1295	48.1	529	4	US-09-912-935-28
4	1295	48.1	529	4	US-09-912-935-40
5	1276	47.4	425	4	US-09-912-935-35
6	1275.5	47.4	530	4	US-09-912-935-38
7	1176.5	43.7	392	4	US-09-764-325A-23
8	1176.5	43.7	392	4	US-09-764-325A-25
9	1176.5	43.7	392	4	US-09-912-935-23
10	1176.5	43.7	392	4	US-09-912-935-25
11	1055	39.2	449	4	US-09-912-935-34
12	115.5	4.3	1568	3	US-09-181-706-2
13	115.5	4.3	1568	3	US-09-458-791-2
14	115.5	4.3	1568	3	US-09-459-066-2
15	115.5	4.3	1568	3	US-09-459-065-2
16	97	3.6	712	4	US-08-543-681A-6132
17	95.5	3.5	3052	2	US-08-557-122A-26
18	95.5	3.5	3052	3	US-09-262-666-26
19	93.5	3.5	1977	4	US-09-976-594-757
20	93.5	3.5	1977	4	US-09-919-039-367
21	93	3.5	1085	1	US-08-431-080-28
22	93	3.5	1085	1	US-08-938-534-28
23	93	3.5	1085	3	US-09-345-294-28
24	92.5	3.4	518	4	US-09-816-248-17
25	92.5	3.4	1220	1	US-08-158-232-43
26	92.5	3.4	1220	2	US-08-611-928-43
27	92.5	3.4	1220	3	US-09-173-891-43

28	90.5	3.4	424	2	US-08-484-993B-18	Sequence 18, Appl
29	90.5	3.4	424	2	US-08-484-158B-18	Sequence 18, Appl
30	90.5	3.4	424	2	US-08-484-596A-18	Sequence 18, Appl
31	90.5	3.4	424	2	US-08-480-150A-18	Sequence 18, Appl
32	90.5	3.4	424	2	US-08-458-731-18	Sequence 18, Appl
33	90.5	3.4	424	2	US-08-149-223A-18	Sequence 18, Appl
34	89.5	3.3	424	6	5169835-6	Patent No. 5169835
35	89.5	3.3	446	4	US-09-252-991A-31114	Sequence 31114, A
36	89	3.3	517	4	US-09-248-796A-14652	Sequence 14652, A
37	89	3.3	595	2	US-08-232-087A-2	Sequence 2, Appl
38	89	3.3	595	3	US-09-006-353A-9	Sequence 9, Appl
39	89	3.3	595	4	US-09-573-986-9	Sequence 9, Appl
40	88.5	3.3	15281	2	US-08-471-119A-2	Sequence 2, Appl
41	88	3.3	490	4	US-09-461-325-250	Sequence 250, App
42	88	3.3	490	4	US-09-461-325-518	Sequence 518, App
43	88	3.3	490	4	US-10-012-542-250	Sequence 250, App
44	88	3.3	490	4	US-10-012-542-518	Sequence 518, App
45	88	3.3	490	4	US-10-115-123-250	Sequence 250, App

ALIGNMENTS

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match	81.2%	Score	2185;	DB	4;	Length	431;
Best Local Similarity	95.2%	Pred. No.	1.3e-209;				
Matches	416;	Conservative	0;	Mismatches	7;	Indels	14;
Gaps	3;						
Qy	72	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTHRQ	131				
Db	1	LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTHRQ	60				
Qy	132	ASRVLSDFDPFFGCHPLRQITATGGIFMGDVIHRLMTATQYVAPLMAFNPCYSDNST	191				
Db	61	ASRVLSDFDPFFGCHPLRQITATGGIFMGDVIHRLMTATQYVAPLMAFNPCYSDNST	120				
Qy	192	VVYFDNGTGVVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQHP	251				
Db	121	VVYFDNGTGVVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQHP	180				
Qy	252	VKTGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSVTSMASVEFTPLPTCLOHRS	311				
Db	181	VKTGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKSVTSMASVEFTPLPTCLOHRS	240				
Qy	312	ACWSSDLTFNCSCWCHVLQRCSSGFDYRQEW-WDYGCAQAEGRMCEDFQD-----ED	363				
Db	241	ACWSSDLTFNCSCWCHVLQRCSSGFDYRQEW-WDYGCAQAEGRMCEDFQD-----ED	294				
Qy	364	HDASPDTSFSPDGDLTITSSSLFIDSLTETDDTKLNPYAGGDLQNNLSPTKGTGPVH	423				
Db	295	TTASPDTSFSPDGDLTITSSSLFIDSLTETDDTKLNPYAGGDLQNNLSPTKGTGPVH	354				
Qy	424	LGTIVGIVLAVLLVAAILLAGIYINGHPTNSAALFFTIERRPHHPAMKFRSHDPHSTYAE	483				

Db 355 LGTIVGIVLAVLLVAAIILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAE 414  
Qy 484 VEPSGHEKEGFMEAEQC 500  
Db 415 VEPSGHEKEGFMEAEQC 431

## RESULT 2

US-09-912-935-31  
; Sequence 31, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: POLYPEPTIDES AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-31

Query Match 48.1%; Score 1295; DB 4; Length 499;  
Best Local Similarity 57.3%; Pred. No. 1.6e-120;  
Matches 250; Conservative 72; Mismatches 166; Indels 8; Gaps 5;  
Qy 72 LAMDTLPDNRTRVVED-NHSYVYSLYGPSPHRELVVDVAEANRSQVKIHTILSNTHR 130  
Db 65 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRLDWNIDQMEKDKVKIHGILSNTHR 124  
Qy 131 QASRVLSFDFPFYGHPLRQITATGFIWGDVHRLMTATQVAPLMANFNPYSDNS 190  
Db 125 QAARVNLSFDFPFYGHFLREITVATGFIYGEVHRMLTATQYIAELMANFDPVSVRNS 184  
Qy 191 TVVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250  
Db 185 TVRFDNGTALVQWDHVLQDNYNLGSFTFQAALLMDGRIFIYKEIPVLVTQISSTNH 244  
Qy 251 PVKTGLSDAFMLNPSDPVPSRRSIFEVHRIELDPKVTSMASAVEFTPLPTCLQHRSC 310  
Db 245 PVKVGSLDAFVVRHRIQQIPNVRRTIYEVHRVQLQMSKITNISAVEMTLPCLQPNRC 304  
Qy 311 DACWSSDLTENCSCWLVQRCSGFDYRQEWMDYCAQAEAGRMCEDFQDEHDSASPD 370  
Db 305 GPCVSSQIGFNCSCWKLQRCSSGFDHRQDWDVDSGCPSESKKMCENTPEVTSRSTTT 364  
Qy 371 T--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424  
Db 365 TIGATTQFRVLVTTTRAVTSQFTSLPTEDDTKIALHLKXNGASTDSDAAEKKGGTILHA 424  
Qy 425 GTTIVGIVLAVLLVAAIILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAEV 484  
Db 425 GLIVGILILVIVATALLVTVMYVHHPTSAASIFFIERRPSRWPMKFRGSGHPAYAEV 484  
Qy 485 EPSGHEKEGFMEAEQC 500  
Db 485 EPVGEKEGFIVSEQC 499

## RESULT 3

US-09-912-935-28  
; Sequence 28, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-28

Query Match 48.1%; Score 1295; DB 4; Length 529;  
Best Local Similarity 57.3%; Pred. No. 1.7e-120;  
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;  
Qy 72 LAMDTLPDNRTRVVED-NHSYVYSLYGPSPHRELVVDVAEANRSQVKIHTILSNTHR 130  
Db 95 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRLDWNIDQMEKDKVKIHGILSNTHR 154  
Qy 131 QASRVLSFDFPFYGHPLRQITATGFIWGDVHRLMTATQVAPLMANFNPYSDNS 190  
Db 155 QAARVNLSFDFPFYGHFLREITVATGFIYGEVHRMLTATQYIAELMANFDPVSVRNS 214  
Qy 191 TVVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250  
Db 215 TVRFDNGTALVQWDHVLQDNYNLGSFTFQAALLMDGRIFIYKEIPVLVTQISSTNH 274  
Qy 251 PVKTGLSDAFMLNPSDPVPSRRSIFEVHRIELDPKVTSMASAVEFTPLPTCLQHRSC 310  
Db 275 PVKVGSLDAFVVRHRIQQIPNVRRTIYEVHRVQLQMSKITNISAVEMTLPCLQPNRC 334  
Qy 311 DACWSSDLTENCSCWLVQRCSGFDYRQEWMDYCAQAEAGRMCEDFQDEHDSASPD 370  
Db 335 GPCVSSQIGFNCSCWKLQRCSSGFDHRQDWDVDSGCPSESKKMCENTPEVTSRSTTT 394  
Qy 371 T--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424  
Db 395 TIGATTQFRVLVTTTRAVTSQFTSLPTEDDTKIALHLKXNGASTDSDAAEKKGGTILHA 454  
Qy 425 GTTIVGIVLAVLLVAAIILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAEV 484  
Db 455 GLIVGILILVIVATALLVTVMYVHHPTSAASIFFIERRPSRWPMKFRGSGHPAYAEV 514  
Qy 485 EPSGHEKEGFMEAEQC 500  
Db 515 EPVGEKEGFIVSEQC 529

## RESULT 4

US-09-912-935-40  
; Sequence 40, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-40

Query Match 48.1%; Score 1295; DB 4; Length 529;



QY 452 TSNAALFPIERRPHHPAMKERSHPDHSYAEVPSGHEKEGFMABOC 500  
Db 483 TSAASIFFPIERRSRPAMKFRSGHPAYAEVPSVG-EKEGFIVSBOC 530

## RESULT 7

US-09-764-325A-23  
; Sequence 23, Application US/09764325A  
; Patent No. 6667391  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Mize, Nancy K.  
; APPLICANT: Childs, John  
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell  
; TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides  
; FILE REFERENCE: 30266/37630A  
; CURRENT APPLICATION NUMBER: US/09/764,325A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/547,358  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 09/545,714  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-325A-23

Query Match 43.7%; Score 1176.5; DB 4; Length 392;  
Best Local Similarity 58.6%; Pred. No. 7.6e-109;  
Matches 229; Conservative 60; Mismatches 95; Indels 7; Gaps 4;

QY 116 RSOVKIHTLSNTHROASRVVLSDFPPYGHPLRQITATGGFIEMGDVHRMLTATQYV 175  
Db 3 KDKVKIHGILSNTHROARVNLSDFFPYGHFLREITVATGGFIYTGVEVHRMLTATQYI 62  
QY 176 APLMANFPGYSDNSTVYFDNGTVFVQMDHVYLVQWEDKSGTFOAALHHDGRIVPAY 235  
Db 63 APLMANFDPVSRSNSTVRYFDNGTALVQMDHVYLVQWEDKSGTFOAALHHDGRIFGY 122  
QY 236 KEIPMSVPEISSOHVPKVTGLSDAFMLNPSDPVPSRRRSIFHYHRIELDPKSVTMSA 295  
Db 123 KEIPVLVTQISSTNHPVKVGLSDAFVVRHRIQIIPNVRRRTIYHYHVELQMSKITNISA 182  
QY 296 VEFTPLPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSGDFDRYQEWMDYGCQAQAEGRM 355  
Db 183 VEMTPLPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSGDFDRYQEWMDYGCQAQAEGRM 355  
QY 356 CEDFQDEHDHDSASPD--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNYPYAGDGLQ 410  
Db 243 CENTPEVETSSRTTTTIGATTQFRVLTTTTRAVTSQFTSLPTEDDTKIALHLKONGAS 302  
QY 411 -NNLSPKTKGTPVHLGTIVGVLVLAAILAGIYINGHPTSNALFFIERRPHHPA 469  
Db 303 TDDSAAEKGGTILHAGLIVGILVILVATAILVTVMYHHPTSAASIFFIERRPSRHPA 362  
QY 470 MKFRSHPDHSTYAEVPSGHEKEGFMABOC 500  
Db 363 MKFRSGHPAYAEVPSVG-EKEGFIVSEOC 392

## RESULT 8

US-09-764-325A-25  
; Sequence 25, Application US/09764325A  
; Patent No. 6667391

## GENERAL INFORMATION:

; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Mize, Nancy K.  
; APPLICANT: Childs, John  
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell  
; TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides  
; FILE REFERENCE: 30266/37630A  
; CURRENT APPLICATION NUMBER: US/09/764,325A  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/547,358  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 09/545,714  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 392  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-325A-25

Query Match 43.7%; Score 1176.5; DB 4; Length 392;

Best Local Similarity 58.6%; Pred. No. 7.6e-109;  
Matches 229; Conservative 60; Mismatches 95; Indels 7; Gaps 4;

QY 116 RSOVKIHTLSNTHROASRVVLSDFPPYGHPLRQITATGGFIEMGDVHRMLTATQYV 175  
Db 3 KDKVKIHGILSNTHROARVNLSDFFPYGHFLREITVATGGFIYTGVEVHRMLTATQYI 62  
QY 176 APLMANFPGYSDNSTVYFDNGTVFVQMDHVYLVQWEDKSGTFOAALHHDGRIVPAY 235  
Db 63 APLMANFDPVSRSNSTVRYFDNGTALVQMDHVYLVQWEDKSGTFOAALHHDGRIFGY 122  
QY 236 KEIPMSVPEISSOHVPKVTGLSDAFMLNPSDPVPSRRRSIFHYHRIELDPKSVTMSA 295  
Db 123 KEIPVLVTQISSTNHPVKVGLSDAFVVRHRIQIIPNVRRRTIYHYHVELQMSKITNISA 182  
QY 296 VEFTPLPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSGDFDRYQEWMDYGCQAQAEGRM 355  
Db 183 VEMTPLPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSGDFDRYQEWMDYGCQAQAEGRM 355  
QY 356 CEDFQDEHDHDSASPD--SFSPYDGLTTTS---SSLFIDSLTTEDDTKLNYPYAGDGLQ 410  
Db 243 CENTPEVETSSRTTTTIGATTQFRVLTTTTRAVTSQFTSLPTEDDTKIALHLKONGAS 302  
QY 411 -NNLSPKTKGTPVHLGTIVGVLVLAAILAGIYINGHPTSNALFFIERRPHHPA 469  
Db 303 TDDSAAEKGGTILHAGLIVGILVILVATAILVTVMYHHPTSAASIFFIERRPSRHPA 362  
QY 470 MKFRSHPDHSTYAEVPSGHEKEGFMABOC 500  
Db 363 MKFRSGHPAYAEVPSVG-EKEGFIVSEOC 392

## RESULT 9

US-09-912-935-23  
; Sequence 23, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912,935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53





	Sequence 2, Application US/09181706	
	Patent No. 6130068	
	GENERAL INFORMATION:	
	APPLICANT: Melanie K. Spriggs, Michael R. Comeau,	
	APPLICANT: Robert F. DuBoise, Richard S. Johnson	
	TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN	
	TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES	
	NUMBER OF SEQUENCES: 10	
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE: Janis C. Henry	
	STREET: 51 University St.	
	CITY: Seattle	
	STATE: WA	
	COUNTRY: US	
	ZIP: 98101	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: Patentin Release #1.0, Version #1.30	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/09/181,706	
	FILING DATE: October 28, 1998	
	CLASSIFICATION:	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US 08/958,598 (converted to a	
	APPLICATION NUMBER: Provisional, see below)	
	FILING DATE: October 28, 1997	
	CLASSIFICATION:	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598	
	APPLICATION NUMBER: conversion to Provisional application)	
	FILING DATE: October 26, 1998	
	CLASSIFICATION:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Henry, Janis C	
	REGISTRATION NUMBER: 34,347	
	REFERENCE/DOCKET NUMBER: 2631-A	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (206)470-4189	
	TELEFAX: (206)233-0644	
	INFORMATION FOR SEQ ID NO: 2:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 1568 amino acids	
	TYPE: amino acid	
	TOPOLOGY: linear	
	MOLECULE TYPE: protein	
	US-09-181-706-2	
	Query Match 4.3%; Score 115.5; DB 3; Length 1568;	
	Best Local Similarity 20.6%; Pred. No. 0.086;	
	Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;	
QY	39 GTVGNRRRARESPGHVSPEPDRT---QLSQDLGGGTLAMDTPDNRTVRVEDNHSSYVS 94	
DB	256 GAATGWPSMAR-----IAQSTEVLFGQAASLDCGHG-----PDGR-----R 292	
QY	95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139	
DB	293 LLLSSSLVEALDVWAGVFSAAGAQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352	
QY	140 -----DPFYGHPRLRQITATCGTFMGDVIHRMLTATQYVAPLMANFNPGYSNDSTVVY 194	
DB	353 HCKEGQPQRPVPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391	
QY	195 FDNGTVFVVQWDHVYLQGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249	
DB	392 LGTG-----DCQLLKVLGENLTSNCFEVIYEKEE 422	
QY	250 HPVKTGLSDAFILNPSPDPVPSRRSRISFEYHRIELDSPKVTSMSSAVEFTPLPTCLOHRS 309	
DB	423 TPV-----FKYLVDP-----VKNIIY-----LTAGEVRRIRIVANCXHKHS 460	

310 CDACMSSDLTFNCSCHVLQRCSGFDRYQE-----WMDYGCAQAEAGRMCEDFQ-----D 367

461 CSECLTA-TDPHCWGCHSLQRCTQCDCVHSENLENWLDI-----SSGAKKCPKIQIRSS 515

362 EDHDSASPDTSFSP 375

516 KEKTIWTMVGSFSP 529

RESULT 13

US-09-458-791-2

; Sequence 2, Application US/09458791

; Patent No. 6174689

; GENERAL INFORMATION:

; APPLICANT: Spriggs, Melanie

; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN

; RECEPTOR DNA AND POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janis C. Henry

; STREET: 51 University St.

; CITY: Seattle

; STATE: WA

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: MS-DOS/Windows 95

; SOFTWARE: Word for Windows 95, 7.0a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/458,791

; FILING DATE: 10-Dec-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/958,598

; FILING DATE: 28-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Henry, Janis C

; REGISTRATION NUMBER: 34,347

; REFERENCE/DOCKET NUMBER: 2631

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)470-4189

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1569 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-458-791-2

Query Match 4.3%; Score 115.5; DB 3; Length 1568;

Best Local Similarity 20.6%; Pred. No. 0.086;

Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20

QY 39 GTVGNRRRARESPGHVSPEPDRT---QLSQDLGGGTLAMDTPDNRTVRVEDNHSSYVS 94

DB 256 GAATGWPSMAR-----IAQSTEVLFGQAASLDCGHG-----PDGR-----R 292

QY 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139

DB 293 LLLSSSLVEALDVWAGVFSAAGAQERRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352

QY 140 -----DPFYGHPRLRQITATCGTFMGDVIHRMLTATQYVAPLMANFNPGYSNDSTVVY 194

DB 353 HCKEGQPQRPVPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391

QY 195 FDNGTVFVVQWDHVYLQGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249

DB 392 LGTG-----DCQLLKVLGENLTSNCFEVIYEKEE 422

QY 250 HPVKTGLSDAFILNPSPDPVPSRRSRISFEYHRIELDSPKVTSMSSAVEFTPLPTCLOHRS 309

DB 423 TPV-----FKYLVDP-----VKNIIY-----LTAGEVRRIRIVANCXHKHS 460



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Db 353 HKEGQDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLP 391
Qy 195 FDNGTVFVQWDHVYLOGWEDKGSFTQOALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
Db 392 LGTG-----DQQLKVLGENLTSNCPEVIYEIKEE 422
Qy 250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRS 309
Db 423 TPV-----FYKLVDP-----VKNIYY-----LTAGKEVRRIRVANCNKHS 460
Qy 310 CDACMSSDLTFNCWCHVLQRCSSGFDYRQE---WMDYGCAQEAEGRMCEQ----D 361
Db 461 CSECLTA-TDPHCGMCHSLQRCCTFGDCVHSENLENWLDI-----SSGAKKCPKIQIIRSS 515
Qy 362 EDHDSASPDTSFSP 375
Db 516 KEKTTVTMTVGSFSP 529
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Search completed: January 28, 2005, 22:14:18  
Job time : 42.8779 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:58 ; Search time 34.626 Seconds  
(without alignments)  
1389.370 Million cell updates/sec

Title: US-09-918-715-230  
Perfect score: 2891  
Sequence: 1 MRGELWLLVLTREARALS.....YAEVPSHGKGFMEAEQC 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	22.7	476	2 T19786	hypothetical prote
2	126	4.7	1161	1 S31213	nidogen precursor
3	115.5	4.3	1568	2 T09074	semaphorin recepto
4	103.5	3.8	979	2 C86446	probable cellulose
5	101.5	3.8	743	2 T09173	EH domain protein
6	101	3.8	733	2 E86345	hypothetical prote
7	100	3.7	535	2 S18606	phosphoenolpyruvat
8	99	3.7	1133	2 T12529	hypothetical prote
9	98	3.6	345	2 T16074	hypothetical prote
10	98	3.6	1502	2 S45429	probable membrane
11	97	3.6	708	2 T83196	NEDD-4 ORF - mouse
12	96.5	3.6	397	2 S33415	corticosteroid-bin
13	96.5	3.6	679	2 T19703	hypothetical prote
14	95.5	3.5	399	1 S71480	homeotic protein H
15	95.5	3.5	887	2 S70642	ubiquitin ligase N
16	95.5	3.5	2120	2 T30243	alpha tectorin - c
17	94	3.5	774	2 JC7265	neprilysin (EC 3.4
18	93.5	3.5	979	1 JC2349	protein-tyrosine-p
19	93.5	3.5	996	2 T48721	PTP 35 protein - m
20	93.5	3.5	1977	2 S54771	sodium channel alp
21	93	3.5	491	2 AG3506	phosphoenolpyruvat
22	92.5	3.5	1085	2 S53352	IFH1 protein - yea
23	92.5	3.4	441	2 JC7653	pectate lyase (EC
24	92.5	3.4	852	2 A85041	probable receptor
25	91.5	3.4	614	2 A98241	hypothetical prote
26	91.5	3.4	614	2 F86088	hypothetical prote
27	91.5	3.4	810	1 F2WMBB	2a protein - broad
28	91.5	3.4	1042	2 A57534	mucin 5AC (clone L
29	91	3.4	633	2 S47144	mating type A prot

30	91	3.4	1175	2 S51005	protein-tyrosine-p
31	90.5	3.4	332	2 JN0067	pregnancy-specific
32	90.5	3.4	424	2 S70399	zona pellucida gly
33	90.5	3.4	4848	2 T30289	pristinamycin I sy
34	90	3.3	561	2 AD2581	phosphoenolpyruvat
35	90	3.3	561	2 B97363	phosphoenolpyruvat
36	90	3.3	798	2 T25104	hypothetical prote
37	90	3.3	1176	2 I58345	protein tyrosine p
38	90	3.3	1179	2 T05673	hypothetical prote
39	90	3.3	1189	2 T51491	hypothetical prote
40	90	3.3	1621	2 T30200	protein-tyrosine k
41	90	3.3	2825	2 T14271	Doc4 protein, stre
42	89.5	3.3	424	2 A34595	pregnancy-specific
43	89.5	3.3	1376	2 G00043	osteonidogen - hum
44	89.5	3.3	1762	2 T03222	probable polyketid
45	89.5	3.3	1840	1 CHRTM1	sodium channel pro

ALIGNMENTS

RESULT 1

T19786

hypothetical protein C36E8.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T19786

R;Wilkinson, J.; Barlow, K.

submitted to the EMBL Data Library, August 1994

A;Reference number: Z19177

A;Accession: T19786

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-476 <WIL>

A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GNO0021; CESP:C3

A;Experimental source: clone C36E8

C;Genetics:

A;Gene: CESP:C36E8.3

A;Map position: 3

A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2

C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 22.7%; Score 611; DB 2; Length 476;

Best Local Similarity 34.2%; Pred. No. 5.6e-42;

Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;

QY	46	RRARES	PGHVSE	PDRTQLS	-----QDLGGGT	LAMD	TL	PD	NK	TR	V	ED	NH	S	V	Y	S	R	L	Y	G	P	S	100	
DB	62	RTAAAP	----	IPKRS	SLASQ	EEDEED	ID	PA	TA	IP	--PD	VE	K	N	D	M	D	H	Q	Y	Q	A	E	T	115
QY	101	EPHSRE	LW	DV	VA	BA	N	R	S	Q	V	K	I	----	HT	I	S	N	T	H	R	O	A	S	156
DB	116	GETLKY	W	I	N	VE	Q	F	M	K	K	P	A	V	G	N	T	S	H	P	L	S	Q	S	175
QY	157	GFIFMG	D	V	I	H	R	M	T	A	T	O	Y	A	P	L	M	A	N	F	N	G	S	D	216
DB	176	GFYIGD	H	S	N	L	A	A	T	O	Y	I	A	P	L	M	A	N	F	H	T	-Y	L	N	234
QY	217	GSTTFO	A	A	L	H	D	G	R	I	V	P	A	K	E	I	P	M	S	V	P	E	I	S	274
DB	235	HSFTFQ	I	L	K	N	G	D	I	V	I	K	D	V	P	D	I	S	N	I	S	D	A	N	291
QY	275	RSIFEV	H	R	I	E	L	D	P	S	K	V	T	S	M	A	V	E	F	T	P	L	P	T	330
DB	292	RVIVEH	R	I	E	A	A	K	I	V	S	N	T	V	I	L	K	A	P	T	C	I	S	P	351
QY	331	--CS	--	S	G	F	R	Y	R	O	E	M	D	Y	C	A	E	A	E	R	M	C	E	-P	384
DB	352	PFCTDE	A	G	L	H	R	R	Q	H	W	F	E	G	N	C	Y	Q	R	S	K	A	L	-P	408
QY	385	SSLFID	S	L	T	T	E	D	D	T	K	L	N	P	Y	A	G	G	D	L	Q	N	N	L	444
DB	409	LPLDAD	R	K	M	K	T	D	T	T	S	D	S	D	E	S	D	E	W	K	H	K	K	E	442

Qy 445 IYINGHP--TSNAALF 458  
Db 443 VATTAPVGTSSQATF 458

RESULT 2  
S31213  
nidogen precursor - sea squirt (Halocynthia roretzi)  
N:Alternate names: entactin  
C:Species: Halocynthia roretzi  
C:Date: 30-Sep-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: S31213  
R:Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.  
Eur. J. Biochem. 213, 11-19, 1993  
A:Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of c  
A:Reference number: S31213; MUID:93238676; PMID:8477687  
A:Accession: S31213  
A:Molecule type: mRNA  
A:Residues: 1-1161 <NAK>  
A:Cross-references: UNIPROT:Q04901; EMBL:D14038; NID:g217363; PIDN:BA03127.1; PID:g2173  
C:Superfamily: Ascidian nidogen; EGF homology; LDL receptor WYTD-containing repeat homol  
C:Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-1161/Product: nidogen #status predicted <MAT>  
F:274-306/Domain: EGF homology <EG1>  
F:560-574/Region: 3-residue repeats (R-P-V)  
F:603-673/Domain: thyroglobulin type I repeat homology <THY1>  
F:686-748/Domain: thyroglobulin type I repeat homology <THY2>  
F:752-819/Domain: thyroglobulin type I repeat homology <THY3>  
F:900-943/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
F:944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
F:987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
F:1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F:1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW5>  
F:1129-1158/Domain: EGF homology <EG2>  
F:107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.7%; Score 126; DB 1; Length 1161;  
Best Local Similarity 23.5%; Pred. No. 0.094;  
Matches 64; Conservative 34; Mismatches 88; Indels 86; Gaps 12;

Qy 137 LSPDFPFVGHPLROITATGGFIEM-----GDVHRLMTATQYVAPLMAN----- 181  
Db 47 LSMPIVFYDKYDSVHTDGFITLENVGADTDGEVL-----LAPFMSDLDTLSG 97

Qy 182 --FNPGYSDNSTVYV-----PDNGTVFVQVMDHYVLOGWEDKGSFTFQAA 224  
Db 98 DIFPREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWVKQSASREDGVFTTFCI 157

Qy 225 LHHGRIVFA---YKEIPMSVPEIS-----SSQHPVKYGLSDA-----FMILNPSP-----DV 269  
Db 158 VATDGAATFAIFLYPODGLAVGENAVKVRNEVTARAGFNDDGREGLEILLSADLLGGDN 217

Qy 270 PESRRRSIFVHRIELDPKSVKTSMSAVEFTPLCTLOHRSACDMSDLTFNCSWCHVLQ 329  
Db 218 AGSQGQIFQGGIMFNNDASKSE-----KH-----HVKK 249

Qy 330 RCSSGFDPRYQEW-MDYGCAQAE-GRMCEDF 359  
Db 250 TRQSGFQVSEVNFEDFNIDLEACGTPCSDF 281

RESULT 3  
T09074  
semaphorin receptor VESPR - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09074  
R:Comeau, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; F  
Immunity 8, 473-482, 1998  
A:Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and b  
A:Reference number: 216555; MUID:98246049; PMID:9586637

A:Accession: T09074  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1568 <COM>  
A:Cross-references: UNIPROT:O60486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3  
A:Experimental source: tissue type foreskin; cell type fibroblast  
C:Genetics:  
A:Gene: VESPR  
C:Keywords: receptor; signal transduction

Query Match 4.3%; Score 115.5; DB 2; Length 1568;  
Best Local Similarity 20.6%; Pred. No. 1;  
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

Qy 39 GTVRGNNRRARSPGHVSEPDRT-----QLSQDLGGGTFLAMDTLPDNRTRVVEDNHSYVS 94  
Db 256 GAATGWPSMAR-----IAQSTEVLFQQAQLDCGHG-----PDGR-----R 292

Qy 95 RLYGPSEPHSRRLWVDV--AEANRSQVKIHTI-----LSNTHRCASRVLSF----- 139  
Db 293 LLLSSSLVEALDVWAGVFAAGEGQRRSPPTTALCLFRMSEIQARAKRVSWDFKTAES 352

Qy 140 -----DPPFYGHPLRQITATGGFIEMGDVHRLMTATQYVAPLMANFNPCYSDNSTVYV 194  
Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391

Qy 195 FDNGTVFVQVMDHYVLOGWEDKGSFTFOAALHHDGRI--VPAYKEIPMSVPEI-----SSSQ 249  
Db 392 LGTG-----DGQLLKVLGENTLSTNCPEVIYEKEE 422

Qy 250 HPVKYGLSDAFMILNPSPDVPESRRRSIFVHRIELDPKSVKTSMSAVEFTPLCTLOHRS 309  
Db 423 TPV-----FYKLVPDP-----VKNIYIY-----LTAGEVRRIRVANCNKHKS 460

Qy 310 CDACMSDLTFNCSWCHVLQRCSSGFDPRYQEW-----WMDYGCAQAEGRMCEDFQ-----D 361  
Db 461 CSECLTA-TDPHCGWCHSLQRCITFGDCVHSENLENWLDI-----SSGAKKPKIQLIRSS 515

Qy 362 EDHDSASPDTSPSP 375  
Db 516 KEKTTVTMVGSPSP 529

RESULT 4  
C86446  
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86446  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86446  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-979 <STO>  
A:Cross-references: UNIPROT:Q9FVR3; GB:AB005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G  
C:Genetics:  
A:Map position: 1

Query Match 3.8%; Score 103.5; DB 2; Length 979;  
Best Local Similarity 21.2%; Pred. No. 5.2;  
Matches 87; Conservative 48; Mismatches 167; Indels 109; Gaps 19;

Qy 4 ELWLLVLVLRRAARALSPQAGHDEGPGGWAAKGTVRGWNNRRAARESPGHVSEPDRTQL 63

Db 342 EKWKHWKVEEDQIKPRPAL---VAPKATWMSDGT--HWPFGTAVSGPHHSRGDHASV 396  
Qy 64 SQDL-----GGTILAMD-----TLPDNRTRVEDNHSYVYVSLRYLGPSEPHSR 105  
Db 397 IQVLDPDPPGDPVKGKGGEGRALDLLEGVDIRLP-----MLVYVREKRPYDHNK 446  
Qy 106 ELWVDVAEANRSQVKIHTILSNTHQASRVVLSFDPPFYGHPLRQITATGGFIFMGDVI 165  
Db 447 K-----AGAMNALVRASAIMSN-----GPFILNLCDDHYVYNSRAF---RDGICFWMDHD 493  
Qy 166 HRLMTATQY-----VAPLMAFNPCYSD-----NSTVYV-F 195  
Db 494 GDRVSYVQFPQRFEGIDPFSRYANKNTVFFDINLRALDGIQGPVYGTGCLFRETALYGF 553  
Qy 196 DNGTVFVVDHVVYVLOGWEDKSTFQAALHHDGRIVFAYKEIPMSV---PEISSQHP- 251  
Db 554 NPPDVFE-----EPPSGSCFP-----LIKRSATVASEPEYTYDDEDR 595  
Qy 252 -----VKTGLSDAFMILNPSDPVPSRRRSIFEYH--RIELDPKVT-SMSAVEFTPLPT 303  
Db 596 FDIGLIRKQFGSSMLVN-SVKVAEFEGRPLATVHSSRLGRPPGSLTGSRRKPLDFATVNE 654  
Qy 304 CLQRSCDACMSSDLTFCNSWCH--VLQRCSSGDFRQEWMDYGCQAQAE 352  
Db 655 AVNVISCWYEDKTEWGFNVGVIYGSVTEDVVTGFRMEHKGWRSPYCVTEPD 705  
RESULT 5  
T09173  
EH domain protein Repsl - mouse  
N;Alternate names: RalBP1-associated EH domain protein Repsl  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09173  
J.Yamaguchi, A.; Urano, T.; Goi, T.; Feig, L.A.  
R. Biol. Chem. 272, 31230-31234, 1997  
A;Title: An eps homology (EH) domain protein that binds to the ral-GTPase target, RalBP1  
A;Reference number: 216602; MUID:98059900; PMID:9395447  
A;Accession: T09173  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-743 <YAM>  
A;Cross-references: UNIPROT:O54916; EMBL:AF031939; NID:G2677842; PIDN:AAB94736.1; PID:G2  
A;Experimental source: cell line: C2C12; tissue type: muscle  
C;Genetics:  
A;Gene: repsl  
C;Keywords: signal transduction  
Query Match 3.8%; Score 101.5; DB 2; Length 743;  
Best Local Similarity 18.3%; Pred. No. 5.1;  
Matches 91; Conservative 63; Mismatches 166; Indels 177; Gaps 23;  
Qy 19 LSPDPGAGH-DEPGSGWAAK-----GTVRGWNRRARESPGHV 55  
Db 78 IPPPPGRGVKGGKSHDAVQRPSEAEQCEPASPWSPQSPPTSPHTWRKHSRPGSGN 137  
Qy 56 SEPRTQLSQ-----DLGGTGLAWDTLPDNRTRVEDNHSYVYVSLRYLGPSEPHSR 109  
Db 138 SERPLTGGPWPSPFGDAQSGSSAGDAV-----WSGSPPPPPQDNWV 179  
Qy 110 DVAE-----ANRSQVKIHTLS-NTHQASRVVLSFPDFPYGHPLRQITAT 155  
Db 180 SPADTPTTSALLTTHPASVQDQTVTRIVASATAANEIRQSSSYEDPW-----KIDTE- 232  
Qy 156 GGFIFMGDVIHRLMTATQY--VAPLMAFNPCYSDNSTVYVVDNGTVFVVDHVVY-LOG 212  
Db 233 -----QRQYVNVQFKTIQPLNGFIPG---SAAKEFFTKSKLPILLSHIWELSD 279  
Qy 213 WEDKGSFT---FOALHHDGRIVFAYK---EIPMSVPEISSQHPVKTGLSDAFMILNPS 266  
Db 280 FDKDGLATLDEFCFAAFH-----LVVARXNGVYDLPEKLPE-----SLMPKLIDLEDS 325

Qy 267 PDVPESRRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFCNSWCH 326  
Db 326 ADVGEQPGVGSYPAAEPSPKSPSPSL-----NQTWPE 361  
Qy 327 VLQRCSSGDFRQEWMDYGCQAQAEGRMCEDFQEDHDSASPDTS----- 372  
Db 362 LNOS-----SEQWETFS-ERSSSQTLTQF-DSNIAPADPDTAIVHPVPIRMTFSKI 411  
Qy 373 -----PSPYDGLTITSSSLFIDSLTDEDTKLNP-----YAGDGLQNLNLS 414  
Db 412 HMQEMELKRTSSDHTNPTSLPVKPSDLSEENKINSSVKPSPGNTVDGYSSSDSPSPD-- 469  
Qy 415 PKTKGTPV-----HLGT 426  
Db 470 PEQIGSSVTRQGRSHSGT 486  
RESULT 6  
E86345  
hypothetical protein FlcF4.9 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: E86345  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso,  
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: E86345  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-733 <STO>  
A;Cross-references: UNIPROT:Q9LMN7; GB:AE005172; NID:G8920637; PIDN:AAF81359.1; GSPDB:GN  
C;Genetics:  
A;Map position: 1  
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot  
Query Match 3.8%; Score 101; DB 2; Length 733;  
Best Local Similarity 24.1%; Pred. No. 5.5;  
Matches 59; Conservative 24; Mismatches 72; Indels 90; Gaps 13;  
Qy 257 SDAFMIILNPSDPVPSRRRSI-----FEYHRIELDPKSVTSMASAVE-FTPLPTCL 305  
Db 139 STGCMSLCDTPPPPNKSCNGVGCCTREVSIPLDSSHRIETQPSRFENMTSVEHFN- 193  
Qy 306 QHRSCD-ACMSSDLTFNCS-----WCHVLQRC-----SS 333  
Db 194 -----CSVAFFVEDGMFNFSLEDLKLQNRVTRPVLVDNIGNQTCQVGVNRTCCGNST 249  
Qy 334 GFDYRQEWMDYGCQAQAEGRM-----CEDFQD---EDHDSASPD-----SF-SPY 376  
Db 250 CFDSRTRKGYNCKLQGFQDGNPVYLDGCDQDINECTTRIHNCSDTSTCENTLGSFHCQCP 309  
Qy 377 DGLTITSSSLFIDSLTDEDTKLNPYAGDGLQNLNLSPTKGTG-TPVHLGTIVIGIVLAVL 435  
Db 310 GSDLNTTMS-CDITPKEE-----PKYLGWTTVLLGTTGTLIGLILL 349  
Qy 436 LVAAL 440  
Db 350 TISYI 354  
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S18606  
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.  
C;Species: Rhizobium sp.  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 27-Oct-2003





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Query Match      3.6%; Score 98; DB 2; Length 1502;
Best Local Similarity 22.7%; Pred.No. 26;
Matches 62; Conservative 41; Mismatches 106; Indels 64; Gaps 14;

Qy      61 TOLSQDLGGGTGLAMDTLPDNRNTRWEDNHYSYVSRLYGPSEPHSRELWVDVAEANSQVK 120
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Db      778 TRLRDIWRGHVFM-TFTDNRV-----TSHAFISS--DPITPSINNLKSDETSONRNI- 829

Qy      121 IHTILSNTHROAGRWVLSPD-FPPYGHPRLQIITIATGCFIFMGDVITHRMILTATYYVAP-L 178
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      830 -----SKVSISKDCIEVY---LSSINILNEFFITYGDSI-----SQISAPVV 868

Qy      179 MANFNPGYDNSIVTVFD-----NGTVFVQWDHVYLQCWEDKGSTFFQAALHHDGRI 231
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      869 LANNNSGRVIDKTVEVANQAESAINAMIKMVQ-----SIKEGLGFNLVLYEESEV 919

Qy      232 -----VFAYKEIPMSVPESISSSHOPVKTKLSDAFMLNPSPDVPESSRRRSIFEYHRIEL 285
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      920 EGFENQYLGFKDI-ISFVSLDVOKDLVKLDKDLF-----APNDKYTSLIRELLISI 970

Qy      286 DPSKVTSMSAVEFTPLPTCLQHRS CDACMSSDL 318
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      971 INRNITKGASIEVT--ATALQRCCGSFCFSASDI 1001


RESULT 11
IR31196
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C:Accession: IR31196
R:Kumar, S.; Tomokawa, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992
A:title: Identification of a set of genes with developmentally down-regulated expression
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**A;Title:** Identification of a set of genes with developmentally down-regulated expression



F:54-167/Domain: protein kinase C C2 region homology <KC2>

F:246-283/Domain: WW repeat homology <WW1>

F:402-439/Domain: WW repeat homology <WW2>

F:459-496/Domain: WW repeat homology <WW3>

F:555-881/Domain: ubiquitin-protein ligase homology <UB1>

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Best Local Similarity 19.2%; Pred. No. 20;
Matches 93; Conservative 55; Mismatches 155; Indels 181; Gaps 25;

Qy 14 EAARALSP-----QPGAG-----HDEGPG-----SGWAKGTVRG-----WNRR 47
Db 218 DQAELEPGVVLQPDADATHLQHPPEPSPLPPGWERQDVLGRTYYVNHESRTQWKP 277
Qy 48 ARES-----FCHVSEPDRTQLSQDLGGGTLMADTLPDNRTR-----VVEDNH 89
Db 278 SPEDDLTDDENGDIQLQAHGAFTTRQISEVDG-----PDHESPENWEIVREDEN 329
Qy 90 SYVYSR-LYGPSEPHSRELWVDVAENRSQVKIHTILSNTHRQASRVVLSFDFPYGHPL 148
Db 330 TIYSGQAVQSPSPGHP-DVQVRLAE-----ELDTLRLT-----MYGNPA 366
Qy 149 RQITATCGGTFMGDVIHRLMTATQYVAPLM-----ANENPGY-----SDNSTVYVFDNGTV 200
Db 367 TSQPVTSNHSRSGSSQTCIFESQPTLPVLPTSSGLPPGWEKQDDRGSRYYVDHNSK 426
Qy 201 FVQWDHYVYLQ-----GWEDKGSFTFQAALHHDGRIVF 233
Db 427 -TTTWSKPTMQDDPRSKIPAHLRGKTPVDSNDLGLPLPGWEER-----THTDGRVFF 477
Qy 234 AYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESR-RRSIFEYHRIELDPKVT 292
Db 478 INHNKTKTQWEDPRMQNVAITG-----PAEPYSRDYKRYEFFFFRKLKKQ---- 522
Qy 293 MSAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLRQCSGSDRYRQEWMDYCAQBAE 352
Db 523 -----TDIPNKFEMK-----LRRAILEDSEYRR-IMGVGRADFLK 556
Qy 353 GRMCEDFQDE---DHDSASPD-----TSFSPYDGDLTSTSSSLFIDSLTTEDDT-KLN 401
Db 557 ARLWIEFDGEGKGLDYGGAWEWFFLISKEMENPYG-----LFEYSATEDNYTLQIN 608
Qy 402 PYAG 405
Db 609 PNSG 612
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Search completed: January 28, 2005, 22:12:46  
Job time : 36.626 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 21:59:20 ; Search time 136.657 Seconds  
(without alignments)  
1321.880 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLVLRARALSPQAGHDEGFGSGWAAKGTVRGWNRRARSPGHVSEPDFR 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2691	100.0	500	10	US-09-918-715-230
2	2691	100.0	500	15	US-10-435-696-79
3	2691	100.0	500	17	US-10-474-794-230
4	2691	100.0	500	17	US-10-357-819-2
5	2691	100.0	1002	10	US-09-918-715-179
6	2691	100.0	1002	17	US-10-474-794-179
7	2602	96.7	488	17	US-10-357-819-4
8	2566	95.4	502	14	US-10-156-487A-5
9	2209	82.1	500	10	US-09-918-715-192
10	2209	82.1	500	10	US-09-918-715-297
11	2209	82.1	500	14	US-10-156-487A-6
12	2209	82.1	500	17	US-10-474-794-192
13	2209	82.1	500	17	US-10-474-794-297

14	2185	81.2	431	10	US-09-912-935-36	Sequence 36, Appl
15	2185	81.2	431	14	US-10-168-365-36	Sequence 36, Appl
16	1295	48.1	499	10	US-09-912-935-31	Sequence 31, Appl
17	1295	48.1	499	14	US-10-168-365-31	Sequence 31, Appl
18	1295	48.1	529	10	US-09-918-715-189	Sequence 189, App
19	1295	48.1	529	10	US-09-918-715-200	Sequence 200, App
20	1295	48.1	529	10	US-09-912-935-28	Sequence 28, Appl
21	1295	48.1	529	10	US-09-912-935-40	Sequence 40, Appl
22	1295	48.1	529	14	US-10-156-487A-4	Sequence 4, Appli
23	1295	48.1	529	14	US-10-168-365-28	Sequence 28, Appl
24	1295	48.1	529	17	US-10-474-794-189	Sequence 189, App
25	1295	48.1	529	17	US-10-474-794-200	Sequence 200, App
26	1294	48.1	529	13	US-10-052-586-472	Sequence 472, App
27	1294	48.1	529	13	US-10-066-500-128	Sequence 128, App
28	1294	48.1	529	14	US-10-174-590-472	Sequence 472, App
29	1294	48.1	529	14	US-10-176-758-472	Sequence 472, App
30	1294	48.1	529	14	US-10-175-737-472	Sequence 472, App
31	1294	48.1	529	14	US-10-174-581-472	Sequence 472, App
32	1294	48.1	529	14	US-10-176-483-472	Sequence 472, App
33	1294	48.1	529	14	US-10-176-749-472	Sequence 472, App
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35	1294	48.1	529	14	US-10-176-915-472	Sequence 472, App
36	1294	48.1	529	14	US-10-173-706-472	Sequence 472, App
37	1294	48.1	529	14	US-10-175-738-472	Sequence 472, App
38	1294	48.1	529	14	US-10-175-752-472	Sequence 472, App
39	1294	48.1	529	14	US-10-176-482-472	Sequence 472, App
40	1294	48.1	529	14	US-10-176-757-472	Sequence 472, App
41	1294	48.1	529	14	US-10-176-913-472	Sequence 472, App
42	1294	48.1	529	14	US-10-180-552-472	Sequence 472, App
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44	1294	48.1	529	14	US-10-173-700-472	Sequence 472, App
45	1294	48.1	529	14	US-10-174-572-472	Sequence 472, App

ALIGNMENTS

RESULT 1

US-09-918-715-230  
; Sequence 230, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 230  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-918-715-230

Query Match 100.0%; Score 2691; DB 10; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.9e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
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Db 481 YAEVPSGHEKEGFMPEAEOC 500

RESULT 2
US-10-435-696-79
; Sequence 79, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-79

Query Match 100.0%; Score 2691; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.9e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 DEDHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLPYAGGDLQNNLSPKTKGT 420
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Db 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
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Db 481 YAEVPSGHEKEGFMPEAEOC 500

RESULT 3
US-10-474-794-230
; Sequence 230, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-230

Query Match 100.0%; Score 2691; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.9e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 60
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Db 121 IHTILSNTHROASRVLSFDPPFGHPLRQITTIATGGFIIMGDVIHRLMTATQVAPLMA 180
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Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 802
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Db 803 LPTCLQHRSCDACMSSDLTFNCSSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCDQ 862
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Db 923 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 983 YAEVPSGHEKEGFMEAEQC 1002

RESULT 6
US-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-179

Query Match 100.0%; Score 2691; DB 17; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1.4e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 60
Db 503 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSPDR 562
Qy 61 TQSQDLGGGTAMDITLDPNTRVVEDNHSYVSRLYGPSPHRELVWDVAEANRSQVK 120
Db 563 TQSQDLGGGTAMDITLDPNTRVVEDNHSYVSRLYGPSPHRELVWDVAEANRSQVK 622
Qy 121 IHTILSNTHQASRVLSFDFPFYGHPLRQITITATGGFIFMGDVIHRMLTATQVAPLMA 180
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Db 623 IHTILSNTHQASRVLSFDFPFYGHPLRQITITATGGFIFMGDVIHRMLTATQVAPLMA 682
Qy 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 683 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 742
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 802
Qy 301 LPTCLQHRSCDACMSSDLTFNCSSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCDQ 360
Db 803 LPTCLQHRSCDACMSSDLTFNCSSCHVLQRCSSGFDYRQEWMDYGCQAEGRMCDQ 862
Qy 361 DEDHDSASPTSFSPYDGLTFTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGT 420
Db 863 DEDHDSASPTSFSPYDGLTFTTSSSLFIDSLLTDDTKLNPYAGDGLQNNLSPKTKGT 922
Qy 421 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 923 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 983 YAEVPSGHEKEGFMEAEQC 1002

RESULT 7
US-10-357-819-4
; Sequence 4, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Baha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
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;; PRIOR APPLICATION NUMBER: 60/359,367  
;; PRIOR FILING DATE: 2002-02-25  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 142  
;; SOFTWARE: CuraseqList version 0.1  
;; SEQ ID NO 4  
;; LENGTH: 488  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-357-819-4

Query Match 96.7%; Score 2602; DB 17; Length 488;  
Best Local Similarity 97.4%; Pred. No. 1.7e-240;  
Matches 487; Conservative 1; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 60  
Db |||||  
Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120  
Db |||||  
Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120  
Db |||||  
Qy 121 IHTILSNTHROASRVLSFDPFPFYGHPLRQITTIATGGFIEMGDVIHMLTATQVAPLMA 180  
Db |||||  
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240  
Db |||||  
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240  
Db |||||  
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEAVFT 300  
Db |||||  
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEAVFT 300  
Db |||||  
Qy 301 LPTCLQRSCDACMSSDLTFNCSCWCHVLRQCSGFDRIYQEW-MDYCAQAEAGRMCEDF 359  
Db |||||  
Qy 361 DEDHDSASPTSFSPYDGLTFTSSSLFIDSLLTDDTKLNPYAGGGLQNNLSPKTKGT 420  
Db |||||  
Qy 421 PVHLGTTIGVILVLAIIAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480  
Db |||||  
Qy 481 YAEVPSGHEKEGFMFAEQ 500  
Db |||||

RESULT 8  
US-10-156-487A-5  
; Sequence 5, Application US/10156487A  
; Publication No. US20030092025A1  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Olinet, John  
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A  
; CURRENT APPLICATION NUMBER: US/10/156,487A  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-156-487A-5

Query Match 95.4%; Score 2566; DB 14; Length 502;  
Best Local Similarity 95.9%; Pred. No. 5e-237;  
Matches 487; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 60  
Db |||||  
Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120  
Db |||||  
Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120  
Db |||||  
Qy 121 IHTILSNTHROASRVLSFDPFPFYGHPLRQITTIATGGFIEMGDVIHMLTATQVAPLMA 180  
Db |||||  
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240  
Db |||||  
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240  
Db |||||  
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEAVFT 300  
Db |||||  
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKVTSMSEAVFT 300  
Db |||||  
Qy 301 LPTCLQRSCDACMSSDLTFNCSCWCHVLRQCSGFDRIYQEW-MDYCAQAEAGRMCEDF 359  
Db |||||  
Qy 360 QD-----EDHDSASPTSFSPYDGLTFTSSSLFIDSLLTDDTKLNPYAGGGLQNN 412  
Db |||||  
Qy 355 QDVRGLPGMRTTTSASPTSFSPYDGLTFTSSSLFIDSLLTDDTKLNPYAGGGLQNN 414  
Db |||||  
Qy 413 LSPKTKGTPVHLGTTIGVILVLAIIAGIYINGHPTSNAAFFIERRPHHPAMK 472  
Db |||||  
Qy 415 LSPKTKGTPVHLGTTIGVILVLAIIAGIYINGHPTSNAAFFIERRPHHPAMK 474  
Db |||||  
Qy 473 RSPDHSTYAEVPSGHEKEGFMFAEQ 500  
Db |||||

RESULT 9  
US-09-918-715-192  
; Sequence 192, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 192  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-918-715-192

Query Match 82.1%; Score 2209; DB 10; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MRGELWLLVLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSEPD 59

Db 1 MRAQLLQLLLLRGAARALSPATPAGHNEQDSAWTAKTRQGSRRPRESPAQVLKPG 60  
Qy 60 RTQLSQDLGGGTGLAMDITLDPNRTVRVEDNHSYYVSRLYGPSEPHSRELWVDVAEANSQV 119  
Db 61 KTQLSQDLGGGSLAIDITLDPNRTVRVEDNHNYYVSRVYGPGEKQSDQLWVDLAVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFFPYGHPRLQITATGGFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRISSSHRQASRVVLSFDFFPYGHPRLQITATGGFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFDNGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVPAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWDHVYLQDREDRGSFTFOAALHRDGRIVFGYKEIP 240  
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFT 299  
Db 241 MAVLDISSAQHPVKAGLSDAFMIILNSPEVPESSRRRTIFEYHRIELDPKVTSMASAVEFT 300  
Qy 300 PLPTCLOHRSQCDTFCVSSNLTFNCSCWCHVLRQCSGFDYRQEWMDYCAQAEAGMCEDF 359  
Db 360 QDEHDHDSASPDTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKG 419  
Qy 361 QDDSHYSASPDSSFPFNGD-STTSSSLFIDSLTTEDDTKLNPYAGDGLPDHSSPKSKG 419  
Db 420 TPVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKMFRSHPDHS 479  
Qy 420 PPVHLGTIVGIVLAVLLVAAILAGIYISGHPNSNAALFFIERRPHHPWPKMFRSHPDHS 479  
Qy 480 TYAEVPSGHEKGFMEAEQC 500  
Db 480 TYTEVPSGHEKGFVEAEQC 500

RESULT 10

US-09-918-715-297  
; Sequence 297, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918.715  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 297  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-918-715-297

Query Match 82.1%; Score 2209; DB 10; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
Qy 1 MRGELWLL-VLVLRGAARALSPQAGHDEGPGSGWAAGTVCWNRRAESPCHVSEPD 59  
Db 1 MRAQLLQLLLLRGAARALSPATPAGHNEQDSAWTAKTRQGSRRPRESPAQVLKPG 60  
Qy 60 RTQLSQDLGGGTGLAMDITLDPNRTVRVEDNHSYYVSRLYGPSEPHSRELWVDVAEANSQV 119  
Db 61 KTQLSQDLGGGSLAIDITLDPNRTVRVEDNHNYYVSRVYGPGEKQSDQLWVDLAVANRSHV 120

Qy 120 KIHTILSNTHROASRVVLSFDFFPYGHPRLQITATGGFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRISSSHRQASRVVLSFDFFPYGHPRLQITATGGFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFDNGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVPAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWDHVYLQDREDRGSFTFOAALHRDGRIVFGYKEIP 240  
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFT 299  
Db 241 MAVLDISSAQHPVKAGLSDAFMIILNSPEVPESSRRRTIFEYHRIELDPKVTSMASAVEFT 300  
Qy 300 PLPTCLOHRSQCDTFCVSSNLTFNCSCWCHVLRQCSGFDYRQEWMDYCAQAEAGMCEDF 359  
Db 360 QDEHDHDSASPDTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKG 419  
Qy 361 QDDSHYSASPDSSFPFNGD-STTSSSLFIDSLTTEDDTKLNPYAGDGLPDHSSPKSKG 419  
Db 420 TPVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKMFRSHPDHS 479  
Qy 420 PPVHLGTIVGIVLAVLLVAAILAGIYISGHPNSNAALFFIERRPHHPWPKMFRSHPDHS 479  
Qy 480 TYAEVPSGHEKGFMEAEQC 500  
Db 480 TYTEVPSGHEKGFVEAEQC 500

RESULT 11

US-10-156-487A-6  
; Sequence 6, Application US/10156487A  
; Publication No. US20030092025A1  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Todd  
; APPLICANT: Bass, Michael B.  
; APPLICANT: Oliner, John  
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof  
; FILE REFERENCE: 01-072-A  
; CURRENT APPLICATION NUMBER: US/10/156,487A  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 60/293,852  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-156-487A-6

Query Match 82.1%; Score 2209; DB 14; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MRGELWLL-VLVLRGAARALSPQAGHDEGPGSGWAAGTVCWNRRAESPCHVSEPD 59  
Db 1 MRAQLLQLLLLRGAARALSPATPAGHNEQDSAWTAKTRQGSRRPRESPAQVLKPG 60  
Qy 60 RTQLSQDLGGGTGLAMDITLDPNRTVRVEDNHSYYVSRLYGPSEPHSRELWVDVAEANSQV 119  
Db 61 KTQLSQDLGGGSLAIDITLDPNRTVRVEDNHNYYVSRVYGPGEKQSDQLWVDLAVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFFPYGHPRLQITATGGFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRISSSHRQASRVVLSFDFFPYGHPRLQITATGGFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFDNGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVPAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWDHVYLQDREDRGSFTFOAALHRDGRIVFGYKEIP 240  
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFT 299

Db 241 MAVLDISSAHPVAGSLSDAFMILNSPEVESQRTTFEYHVELDSSKITTTSAVEFT 300  
Qy 300 PLPTCLQHRSCDACWSSDLTFNCSCWCHVLRQCSGGFDRYRQEMMDYGCACAEAGRMCEDF 359  
Db 301 PLPTCLQHQSCDTCVSSNLTFCNSWCHVLRQCSGGFDRYRQEWLTYGCAEAEKTCEDF 360  
Qy 360 QDEHDSASPTSPSPVDGDLTTSSSLFDLSLTEDDTKLNPNYAGDGLONNLSPTKKG 419  
Db 361 QDDSHYSASPDSSFPNGD-STTSSSLFDLSLTEDDTKLNPNYAGDGLPDHSSPSKSG 419  
Qy 420 TPVHLGTIVGIVLAVLVAAILAGIYINGHPTSNAAALFFIERRPHPWPAKPFHSDHS 479  
Db 420 PPVHLGTIVGIVLAVLVAAILAGIYISGHPNSNAALFFIERRPHPWPAKPFHSDHS 479  
Qy 480 TYAEVPSGHEKEGFMEAEQC 500  
Db 480 TYTEVEPSGHEKEGFVEAEQC 500

RESULT 12  
US-10-474-794-192  
; Sequence 192, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-474-794-192

Query Match 82.1%; Score 2209; DB 17; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
Qy 1 MRGELWLL-VLVLREAAARALSPQAGHDEGPGSGWAAKGTVRGWNRRARSPGHVSEPD 59  
Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEQDSAWTAKTRQCSWRRRSPSPAQLKPG 60  
Qy 60 RTQLSODLGGTTLAMDTPNRTVRVEDNHSYVSRLYGPSEPHSRRLVWDVAANRSQV 119  
Db 61 KTQLSODLGGSLAIDTPNRTVRVEDNHNHYVSRVYGPGEKQSDQLWDLVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGCFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRILSSSHRQASRVVLSFDFPFYGHPLRQITITATGCFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIP 239  
Db 61 KTQLSODLGGSLAIDTPNRTVRVEDNHNHYVSRVYGPGEKQSDQLWDLVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGCFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRILSSSHRQASRVVLSFDFPFYGHPLRQITITATGCFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWHDVYLQDREDRGSFTFQAALHHDGRIVFAYKEIP 240  
Qy 240 MSVPEISSSQHPVKTLGSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASVEFT 299  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWHDVYLQDREDRGSFTFQAALHHDGRIVFAYKEIP 240  
Qy 240 MSVPEISSSQHPVKTLGSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASVEFT 299  
Db 241 MAVLDISSAHPVAGSLSDAFMILNSPEVESQRTTFEYHVELDSSKITTTSAVEFT 300  
Qy 300 PLPTCLQHRSCDACWSSDLTFNCSCWCHVLRQCSGGFDRYRQEMMDYGCACAEAGRMCEDF 359  
Db 301 PLPTCLQHQSCDTCVSSNLTFCNSWCHVLRQCSGGFDRYRQEWLTYGCAEAEKTCEDF 360

Qy 360 QDEHDSASPTSPSPVDGDLTTSSSLFDLSLTEDDTKLNPNYAGDGLONNLSPTKKG 419  
Db 361 QDDSHYSASPDSSFPNGD-STTSSSLFDLSLTEDDTKLNPNYAGDGLPDHSSPSKSG 419  
Qy 420 TPVHLGTIVGIVLAVLVAAILAGIYINGHPTSNAAALFFIERRPHPWPAKPFHSDHS 479  
Db 420 PPVHLGTIVGIVLAVLVAAILAGIYISGHPNSNAALFFIERRPHPWPAKPFHSDHS 479  
Qy 480 TYAEVPSGHEKEGFMEAEQC 500  
Db 480 TYTEVEPSGHEKEGFVEAEQC 500

RESULT 13  
US-10-474-794-297  
; Sequence 297, Application US/10474794  
; Publication No. US20040213793A1  
; GENERAL INFORMATION:  
; APPLICANT: Carson-Walter, Eleanor  
; APPLICANT: St. Croix, Brad  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00179  
; CURRENT APPLICATION NUMBER: US/10/474,794  
; CURRENT FILING DATE: 2003-10-14  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/308,829  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 359  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 297  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Mouse  
US-10-474-794-297

Query Match 82.1%; Score 2209; DB 17; Length 500;  
Best Local Similarity 81.6%; Pred. No. 9.6e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
Qy 1 MRGELWLL-VLVLREAAARALSPQAGHDEGPGSGWAAKGTVRGWNRRARSPGHVSEPD 59  
Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEQDSAWTAKTRQCSWRRRSPSPAQLKPG 60  
Qy 60 RTQLSODLGGTTLAMDTPNRTVRVEDNHSYVSRLYGPSEPHSRRLVWDVAANRSQV 119  
Db 61 KTQLSODLGGSLAIDTPNRTVRVEDNHNHYVSRVYGPGEKQSDQLWDLVANRSHV 120  
Qy 120 KIHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGCFIFMGDVIHRMLTATQYVAPLM 179  
Db 121 KIHRILSSSHRQASRVVLSFDFPFYGHPLRQITITATGCFIFMGDMLHRMLTATQYVAPLM 180  
Qy 180 ANFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIP 239  
Db 181 ANFNPGYSDNSTVAYFDNGTVFVQWHDVYLQDREDRGSFTFQAALHHDGRIVFAYKEIP 240  
Qy 240 MSVPEISSSQHPVKTLGSDAFMILNPSDPVPESSRRSIFEYHRIELDPKVTSMASVEFT 299  
Db 241 MAVLDISSAHPVAGSLSDAFMILNSPEVESQRTTFEYHVELDSSKITTTSAVEFT 300  
Qy 300 PLPTCLQHRSCDACWSSDLTFNCSCWCHVLRQCSGGFDRYRQEMMDYGCACAEAGRMCEDF 359  
Db 301 PLPTCLQHQSCDTCVSSNLTFCNSWCHVLRQCSGGFDRYRQEWLTYGCAEAEKTCEDF 360  
Qy 360 QDEHDSASPTSPSPVDGDLTTSSSLFDLSLTEDDTKLNPNYAGDGLONNLSPTKKG 419  
Db 361 QDDSHYSASPDSSFPNGD-STTSSSLFDLSLTEDDTKLNPNYAGDGLPDHSSPSKSG 419  
Qy 420 TPVHLGTIVGIVLAVLVAAILAGIYINGHPTSNAAALFFIERRPHPWPAKPFHSDHS 479  
Db 420 PPVHLGTIVGIVLAVLVAAILAGIYISGHPNSNAALFFIERRPHPWPAKPFHSDHS 479

Qy 480 TYAEVPSGHEKEGFMEAEQC 500  
Db 480 TYTEVPSGHEKEGFMEAEQC 500

## RESULT 14

US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Publication No. US20030022825A1  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsu et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match 81.2%; Score 2185; DB 10; Length 431;  
Best Local Similarity 95.2%; Pred. No. 1.5e-200;  
Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	72	LAMDTLPDNRTRVVDNHSYVSRLYGSPSPHSRELWVDVAEANSQVKIHTILSNTHRQ	131
Db	1	LAMDTLPDNRTRVVDNHSYVSRLYGSPSPHSRELWVDVAEANSQVKIHTILSNTHRQ	60
Qy	132	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	191
Db	61	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	120
Qy	192	VVYFDNGTVFVQWDHVVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	251
Db	121	VVYFDNGTVFVQWDHVVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	180
Qy	252	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	311
Db	181	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	240
Qy	312	ACMSDDLTFNCWCHVLQRCSSGFDYRQEW-MDYGCAQAEGRMCEDFQD-----ED	363
Db	241	ACMSDDLTFNCWCHVLQRCSSGFDYRQEWDMGTGCAQAEAG-----QDVRGLPGMRT	294
Qy	364	HDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	423
Db	295	TTSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	354
Qy	424	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHSTYAE	483
Db	355	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHSTYAE	414
Qy	484	VEPSGHEKEGFMEAEQC 500	
Db	415	VEPSGHEKEGFMEAEQC 431	

## RESULT 15

US-10-168-365-36  
; Sequence 36, Application US/10168365  
; Publication No. US20030211987A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Childs, John

; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Mize, Nancy  
; APPLICANT: Lee, Juhl  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 30266/37630  
; CURRENT APPLICATION NUMBER: US/10/168,365  
; CURRENT FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-365-36

Query Match 81.2%; Score 2185; DB 14; Length 431;  
Best Local Similarity 95.2%; Pred. No. 1.5e-200;  
Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy	72	LAMDTLPDNRTRVVDNHSYVSRLYGSPSPHSRELWVDVAEANSQVKIHTILSNTHRQ	131
Db	1	LAMDTLPDNRTRVVDNHSYVSRLYGSPSPHSRELWVDVAEANSQVKIHTILSNTHRQ	60
Qy	132	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	191
Db	61	ASRVVLSDFDPFGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST	120
Qy	192	VVYFDNGTVFVQWDHVVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	251
Db	121	VVYFDNGTVFVQWDHVVYVQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP	180
Qy	252	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	311
Db	181	VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSCD	240
Qy	312	ACMSDDLTFNCWCHVLQRCSSGFDYRQEW-MDYGCAQAEGRMCEDFQD-----ED	363
Db	241	ACMSDDLTFNCWCHVLQRCSSGFDYRQEWDMGTGCAQAEAG-----QDVRGLPGMRT	294
Qy	364	HDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	423
Db	295	TTSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGDGLQNNLSPKTKGTPVH	354
Qy	424	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHSTYAE	483
Db	355	LGTIVGIVLAVLLVAAILLAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHSTYAE	414
Qy	484	VEPSGHEKEGFMEAEQC 500	
Db	415	VEPSGHEKEGFMEAEQC 431	

Search completed: January 28, 2005, 22:19:22  
Job time : 138.657 secs

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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:52:02 ; Search time 158.818 Seconds  
(without alignments)  
1129.372 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691  
Sequence: 1 MRGELWLLVLVLRARALs.....YAEVPSGKKGPMKMEAEQC 500

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2691	100.0	500	5	ABb90749 Human Tum
2	2691	100.0	500	6	ABu54456 Human tum
3	2691	100.0	500	7	ADi21063 Novel hum
4	2691	100.0	500	8	ADh13230 Human mal
5	2691	100.0	527	7	ADi21554 Novel hum
6	2691	100.0	527	7	ADi21553 Novel hum
7	2691	100.0	1002	5	ABb90723 Human Tum
8	2691	100.0	1002	6	ABu54430 Human tum
9	2607	96.9	488	7	ADi21064 Novel hum
10	2209	82.1	500	5	ABb90783 Mouse Tum
11	2209	82.1	500	5	ABb90729 Mouse Tum
12	2209	82.1	500	6	ABu54436 Mouse tum
13	2209	82.1	500	6	ABu54490 Mouse tum
14	2185	81.2	431	4	AAb85400 Tumour en
15	2185	81.2	431	6	ABO01434 Human tum
16	2007	74.6	400	3	AAb43131 Human ORF
17	1295	48.1	499	4	AAb85396 Stem cell
18	1295	48.1	499	6	ABO01430 Human ste
19	1295	48.1	529	4	AAb85394 Stem cell
20	1295	48.1	529	5	ABb90734 Human Tum
21	1295	48.1	529	5	ABb90726 Human Tum
22	1295	48.1	529	5	ABp53349 Human tra
23	1295	48.1	529	5	ABg69157 Human ste
24	1295	48.1	529	5	ABg69161 Human pro
25	1295	48.1	529	6	ABu54441 Human tum

26	1295	48.1	529	6	ABU54433	Human tum
27	1295	48.1	529	6	ABO01436	Human ste
28	1295	48.1	529	6	ABO01428	Human ste
29	1295	48.1	529	6	AAE35354	Human TEM
30	1295	48.1	529	8	ADN05749	Antipsoi
31	1294	48.1	529	4	AAb31211	Amino aci
32	1294	48.1	529	4	AAU29259	Human PRO
33	1294	48.1	529	4	AAU39068	Human PRO
34	1294	48.1	529	6	ABU58635	Human PRO
35	1294	48.1	529	6	ABU88183	Novel hum
36	1294	48.1	529	6	ABU84498	Human sec
37	1294	48.1	529	6	ABR66372	Human sec
38	1294	48.1	529	6	ABR65762	Human sec
39	1294	48.1	529	6	ABU99702	Human sec
40	1294	48.1	529	6	ABU82941	Human PRO
41	1294	48.1	529	6	ABU90062	Novel hum
42	1294	48.1	529	6	ABR68311	Human hum
43	1294	48.1	529	6	ABU96364	Novel hum
44	1294	48.1	529	6	ABU92795	Human sec
45	1294	48.1	529	6	ABO08872	Human sec

ALIGNMENTS

RESULT 1  
ABB90749  
ID ABB90749 standard; protein; 500 AA.  
XX  
AC ABB90749;  
XX  
DT 30-MAY-2002 (first entry)  
XX  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.  
XX  
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.  
XX  
OS Homo sapiens.  
XX  
FN WO200210217-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 01-AUG-2001; 2001WO-US024031.  
XX  
PR 02-AUG-2000; 2000US-0222599P.  
PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI St Croix B, Kinzler KW, Vogelstein B;  
XX  
DR WPI: 2002-291856/33.  
XX  
DR N-PSDB; ABL92103.  
XX  
PT An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
PS Claim 1; Page 206-207; 31pp; English.  
XX  
CC The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic

CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 5; Length 500;  
Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
Qy 61 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
Db 61 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120  
Qy 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDVHRLMLTATQYVAPLMA 180  
Db 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDVHRLMLTATQYVAPLMA 180  
Qy 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
Db 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240  
Qy 241 SVPEISSQHPVKTGSLDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTP 300  
Db 241 SVPEISSQHPVKTGSLDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTP 300  
Qy 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQSSGFDRYRQEWMDYGCQAEGRMCSDFQ 360  
Db 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQSSGFDRYRQEWMDYGCQAEGRMCSDFQ 360  
Qy 361 DEHDHSDPSTSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
Db 361 DEHDHSDPSTSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420  
Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480  
Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 481 YAEVEPSGHEKEGFMEAEQC 500

RESULT 2  
ABUS4456  
ID ABUS4456 standard; protein; 500 AA.

XX  
XX AC ABUS4456;

XX  
XX DT 12-MAR-2003 (first entry)

XX  
XX DE Human tumour endothelial marker TEM 17.

XX  
XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
XX Tumour endothelial marker; normal endothelial marker; PEM;  
XX pan-endothelial marker; polycystic kidney disease; psoriasis;  
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
XX neovascularization; immune response; cytostatic; antidiabetic;  
XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX  
XX OS Homo sapiens.

XX  
XX FN WO200283874-A2.

XX  
XX PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US008253.  
XX  
XX PR 11-APR-2001; 2001US-0282850P.  
XX PR 06-FEB-2002; 2002US-0354262P.  
XX  
XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX  
XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
XX  
XX DR WPT; 2003-093016/08.  
XX DR N-PSDB; ABX72028.

XX  
XX PT New purified human transmembrane protein, designated as tumor endothelial  
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
XX psoriasis.

XX  
XX PS Disclosure; Page 221-222; 374pp; English.

XX  
XX CC The present invention relates to a novel method for the isolation of  
XX endothelial cells (ECs), and the identification of genes expressed in  
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal  
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
XX identified in human ECs. The human EC marker proteins and the  
XX polynucleotide sequences encoding them are useful for detecting,  
XX diagnosing or treating tumours as well as polycystic kidney disease,  
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
XX useful for inhibiting neovascularization or tumour angiogenesis, for  
XX inducing an immune response to tumour endothelial cells in a patient, or  
XX for identifying candidate drugs for treating tumours. The present  
XX sequence represents a human TEM or NEM protein of the invention

XX  
XX SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 6; Length 500;  
Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60  
Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSPDR 60

Qy 61 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120

Db 61 TQLSQDLGGGTAMDITLPDNRTRVEDNHSYVVSRLYGPSEPHSRELWVDVAEANRSQVK 120

Qy 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDVHRLMLTATQYVAPLMA 180

Db 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDVHRLMLTATQYVAPLMA 180

Qy 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

Db 181 NFNPYSDNSTVYVFDNGTVVQWMDHYVLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTGSLDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTP 300

Db 241 SVPEISSQHPVKTGSLDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMGSAVEFTP 300

Qy 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQSSGFDRYRQEWMDYGCQAEGRMCSDFQ 360

Db 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLRQSSGFDRYRQEWMDYGCQAEGRMCSDFQ 360

Qy 361 DEHDHSDPSTSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420

Db 361 DEHDHSDPSTSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420

Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480

Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480

Qy 481 YAEVEPSGHEKEGFMEAEQC 500

Db 481 YAEVEPSGHEKEGFMEAEQC 500

RESULT 3  
ADI21063  
ID ADI21063 standard; protein; 500 AA.  
XX  
XX  
AC ADI21063;  
XX  
DT 15-APR-2004 (first entry)  
XX  
XX  
DE Novel human protein #38.  
XX  
XX forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX  
XX  
OS Homo sapiens.  
XX  
XX WO2003025148-A2.  
XX  
XX  
PD 27-MAR-2003.  
XX  
XX 19-SEP-2002; 2002WO-US029964.  
XX  
XX 19-SEP-2001; 2001US-0323739P.  
XX  
XX 13-SEP-2002; 2002US-00323739.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX  
XX WPI; 2003-354603/33.  
DR  
DR N-PSDB; ADI21779.  
XX  
XX  
PT New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX  
XX Claim 20; SEQ ID NO 314; 156pp; English.  
XX  
XX The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping, and  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC protein.  
XX  
XX  
SQ Sequence 500 AA;  
Query Match 100.0%; Score 2691; DB 7; Length 500;  
Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60  
DB 1 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSEPD 60  
QY 61 TQLSQDLGGGTAMDITLDPNRTVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120

Db 61 TQLSQDLGGGTAMDITLDPNRTVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120  
QY 121 IHTILSNTHRQASRVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180  
Db 121 IHTILSNTHRQASRVLSFDFFPYGHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180  
QY 181 NFNGYSDNSTVYVFDNGTVFVQWHDHVLQGWEDKGSFTFQAALHHDGRIVFAYPEIPM 240  
Db 181 NFNGYSDNSTVYVFDNGTVFVQWHDHVLQGWEDKGSFTFQAALHHDGRIVFAYPEIPM 240  
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRERSIFEYHRIELDPKVTSMGSAVEFTP 300  
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRERSIFEYHRIELDPKVTSMGSAVEFTP 300  
QY 301 LPTCLQHRSCDACSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAQEAEGRMCEDFQ 360  
Db 301 LPTCLQHRSCDACSSDLTFNCSCWCHVLQRCSSGFDRYQEWMDYGCQAQEAEGRMCEDFQ 360  
QY 361 DEHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
Db 361 DEHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
QY 421 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480  
Db 421 PVHLGTTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480  
QY 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 481 YAEVEPSGHEKEGFMEAEQC 500  
RESULT 4  
ADH13230  
ID ADH13230 standard; protein; 500 AA.  
XX  
XX AC ADH13230;  
XX  
XX 11-MAR-2004 (first entry)  
DT Human malignant neoplasia-related protein SeqID79.  
DE  
XX malignant neoplasia; cytostatic; breast cancer; ovarian cancer;  
KW gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;  
KW bladder cancer; non-small cell lung cancer; human.  
XX  
XX Homo sapiens.  
XX  
XX EPI365034-A2.  
XX  
XX 26-NOV-2003.  
XX  
XX 09-MAY-2003; 2003EP-00010447.  
XX  
XX 21-MAY-2002; 2002EP-00010291.  
XX  
XX 13-FEB-2003; 2003EP-00003112.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Wirtz R, Munnes M, Kallabis H;  
XX  
XX WPI; 2004-073279/08.  
DR  
DR N-PSDB; ADH13207.  
XX  
XX  
PT Predicting, diagnosing or prognosing malignant neoplasia by detecting at  
PT least two markers, where the markers are genes from one or more  
PT chromosomal regions altered in malignant neoplasia.  
XX  
XX  
PS Claim 11; SEQ ID NO 79; 267pp; English.  
XX  
XX  
CC This invention relates to a novel method for the prediction, diagnosis,  
CC or prognosis of malignant neoplasia by the detection of at least two  
CC markers. The invention may also be useful for the development of

cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia, such as breast cancer, ovarian cancer, gastric cancer, colon cancer, oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell lung cancer. The polynucleotides and polypeptides defined in the specification, antisense polynucleotides targeting the polynucleotides, antibodies targeting either one of the polynucleotides or polypeptides, and compounds identified by the screening methods are useful for preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method of the invention.

XX Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 8; Length 500;  
Best Local Similarity 100.0%; Pred. No. 3.1e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60  
Db 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60  
Qy 61 TQLSODLGGGTAMDITLDPNRTVRVEDNHSYVVSRLYGPSPHRELWVDVAEANRSQVK 120  
Db 61 TQLSODLGGGTAMDITLDPNRTVRVEDNHSYVVSRLYGPSPHRELWVDVAEANRSQVK 120  
Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIFMGDVHRLMTATQVAPLMA 180  
Db 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIFMGDVHRLMTATQVAPLMA 180  
Qy 181 NFNGYSDNSTVYVFDNGTGVVQWDHVYLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 240  
Db 181 NFNGYSDNSTVYVFDNGTGVVQWDHVYLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 240  
Qy 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPSKVTSMASAVEFTP 300  
Db 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPSKVTSMASAVEFTP 300  
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360  
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360  
Qy 361 DEDHDSASPDTSFSPYDGDITTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420  
Db 361 DEDHDSASPDTSFSPYDGDITTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420  
Qy 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALEFFIERRPHHPAMKFRSHPDHST 480  
Db 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALEFFIERRPHHPAMKFRSHPDHST 480  
Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 481 YAEVEPSGHEKEGFMEAEQC 500

RESULT 5

ADI21554

ID ADI21554 standard; protein; 527 AA.

XX

AC ADI21554;

XX

DT 15-APR-2004 (first entry)

XX

DE Novel human polypeptide #33.

XX

KW forensic; nutritional source; damaged tissue; diseased tissue;

KW myeloid cell disorder; lymphoid cell disorder;

KW bone cartilage tissue growth; tendon tissue growth;

KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;

KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

XX

OS Homo sapiens.

XX

PN WO2003025148-A2.

XX

PD 27-MAR-2003.

XX

PF 19-SEP-2002; 2002WO-US029964.

XX

PR 19-SEP-2001; 2001US-0323739P.

XX

PR 13-SEP-2002; 2002US-00323739.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;

PI Haley-Vicente D;

XX

DR WPI; 2003-354603/33.

XX

DR N-PSDB; ADI21334.

XX

PT New polynucleotides and secreted proteins, useful for treating myeloid or

PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve

PT tissue growth or regeneration, in wound healing, and in tissue repair and

PT replacement.

XX

PS Example 3; SEQ ID NO 805; 156pp; English.

XX

CC The invention relates to an isolated polynucleotide encoding a

CC polypeptide with biological activity. The polynucleotides and

CC polypeptides are useful in diagnostics, forensics, gene mapping,

CC identification of mutations responsible for genetic disorders and other

CC traits, to assess biodiversity, as nutritional sources or supplements.

CC The polynucleotides may also be used as molecular weight markers,

CC chromosome markers or map related gene positions, or as an antigen to

CC raise anti-DNA antibodies or elicit immune response. The polypeptides are

CC useful for raising antibodies, as markers for tissues in which the

CC corresponding polypeptide is expressed, for re-engineering damaged or

CC diseased tissues, for treating myeloid or lymphoid cell disorders, in

CC bone cartilage, tendon, ligament and/or nerve tissue growth or

CC regeneration, in wound healing, in tissue repair and replacement, in

CC healing of burns, incisions and ulcers, and in treating cancer. The

CC present sequence represents the amino acid sequence of a novel human

CC polypeptide.

XX

SQ Sequence 527 AA;

XX

Query Match 100.0%; Score 2691; DB 7; Length 527;

Best Local Similarity 100.0%; Pred. No. 3.3e-249;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60

Db 28 MRGELWLLVLVLEAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 87

Qy 61 TQLSODLGGGTAMDITLDPNRTVRVEDNHSYVVSRLYGPSPHRELWVDVAEANRSQVK 120

Db 88 TQLSODLGGGTAMDITLDPNRTVRVEDNHSYVVSRLYGPSPHRELWVDVAEANRSQVK 147

Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIFMGDVHRLMTATQVAPLMA 180

Db 148 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIFMGDVHRLMTATQVAPLMA 207

Qy 181 NFNGYSDNSTVYVFDNGTGVVQWDHVYLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 240

Db 208 NFNGYSDNSTVYVFDNGTGVVQWDHVYLOGWEDKGSFTQAAALHHDGRIVFAYKEIPM 267

Qy 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPSKVTSMASAVEFTP 300

Db 268 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPSKVTSMASAVEFTP 327

Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 360

Db 328 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQ 387



Qy 361 DEDHDSASPTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
Db 388 DEDHDSASPTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 447  
Qy 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
Db 448 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507  
Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 508 YAEVEPSGHEKEGFMEAEQC 527

RESULT 6  
ADI21553  
ID ADI21553 standard; protein; 527 AA.  
AC ADI21553;  
XX 15-APR-2004 (first entry)  
XX Novel human polypeptide #32.  
XX forensic; nutritional source; damaged tissue; diseased tissue;  
KW myeloid cell disorder; lymphoid cell disorder;  
KW bone cartilage tissue growth; tendon tissue growth;  
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.  
XX Homo sapiens.  
XX WO2003025148-A2.  
XX 27-MAR-2003.  
XX 19-SEP-2002; 2002WO-US029964.  
XX 19-SEP-2001; 2001US-0323739P.  
XX 13-SEP-2002; 2002US-00323739.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
PI Haley-Vicente D;  
XX WPI; 2003-354603/33.  
DR N-PSDB; ADI21333.  
XX New polynucleotides and secreted proteins, useful for treating myeloid or  
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
PT tissue growth or regeneration, in wound healing, and in tissue repair and  
PT replacement.  
XX Example 3; SEQ ID NO 804; 156pp; English.  
XX The invention relates to an isolated polynucleotide encoding a  
CC polypeptide with biological activity. The polynucleotides and  
CC polypeptides are useful in diagnostics, forensics, gene mapping, and  
CC identification of mutations responsible for genetic disorders and other  
CC traits, to assess biodiversity, as nutritional sources or supplements.  
CC The polynucleotides may also be used as molecular weight markers,  
CC chromosome markers or map related gene positions, or as an antigen to  
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
CC useful for raising antibodies, as markers for tissues in which the  
CC corresponding polypeptide is expressed, for re-engineering damaged or  
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
CC regeneration, in wound healing, in tissue repair and replacement, in  
CC healing of burns, incisions and ulcers, and in treating cancer. The  
CC present sequence represents the amino acid sequence of a novel human  
CC polypeptide.

XX SQ Sequence 527 AA;  
Query Match 100.0%; Score 2691; DB 7; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3 3e-249;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRGELWLLVLVLEAARALSPQCGAGHDEGPGSGAAAKGTVRGNRRARSPGHVSEPR 60  
Db 28 MRGELWLLVLVLEAARALSPQCGAGHDEGPGSGAAAKGTVRGNRRARSPGHVSEPR 87  
Qy 61 TQLSODLGGGTLMADTLPDNRTRVEDNHSYVYSLYGPSEPHSRELWVDVAENRSQVK 120  
Db 88 TQLSODLGGGTLMADTLPDNRTRVEDNHSYVYSLYGPSEPHSRELWVDVAENRSQVK 147  
Qy 121 IHTILSNTHROASRVLSFDFFPYGHPRLQITATGCFIPMGDVIHRMLTATQVAPLMA 180  
Db 148 IHTILSNTHROASRVLSFDFFPYGHPRLQITATGCFIPMGDVIHRMLTATQVAPLMA 207  
Qy 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 240  
Db 208 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 267  
Qy 241 SVPEISSQHPVKLTGLSDAFMILNPSDPVPSRRSIFEYHRIELDPSKVTMSAVEFTP 300  
Db 268 SVPEISSQHPVKLTGLSDAFMILNPSDPVPSRRSIFEYHRIELDPSKVTMSAVEFTP 327  
Qy 301 LPTCLQHRSCDACSSDLTFNCSCWCHVLQRCSSGFDYRQWMDYGCQAEGRMCEDFQ 360  
Db 328 LPTCLQHRSCDACSSDLTFNCSCWCHVLQRCSSGFDYRQWMDYGCQAEGRMCEDFQ 387  
Qy 361 DEDHDSASPTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
Db 388 DEDHDSASPTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 447  
Qy 421 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
Db 448 PVHLGTTIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507  
Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
Db 508 YAEVEPSGHEKEGFMEAEQC 527

RESULT 7  
ABB90723  
ID ABB90723 standard; protein; 1002 AA.  
XX AC ABB90723;  
XX 30-MAY-2002 (first entry)  
DT Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.  
DE Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
KW psoriasis.  
XX Homo sapiens.  
XX WO200210217-A2.  
PD 07-FEB-2002;  
XX 01-AUG-2001; 2001WO-US024031.  
PF 02-AUG-2000; 2000US-0222599P.  
PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA

XX St Croix B, Kinzler KW, Vogelstein B;  
 XX WPI; 2002-291856/33.  
 XX  
 XX An isolated molecule comprising an antibody variable region which  
 PT specifically binds to an extracellular domain of a tumor endothelial  
 PT marker (TEM) protein, useful for inhibiting tumor growth.  
 XX  
 XX Disclosure; Page 125-128; 331pp; English.  
 XX  
 CC The invention relates to an isolated molecule comprising an antibody  
 CC variable region which specifically binds to an extracellular domain of a  
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
 CC are disclosed, as are marker oligonucleotide sequences: tumour  
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
 CC (PEM) ABL91903-ABL91995  
 XX  
 SQ Sequence 1002 AA;  
 Query Match 100.0%; Score 2691; DB 5; Length 1002;  
 Best Local Similarity 100.0%; Pred. No. 9e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRGELLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 60  
 Db |||||||||  
 Qy 503 MRGELLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 562  
 Db |||||||||  
 Qy 61 TQSQDLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGSPSPHSELVWDVAEANRSQVK 120  
 Db |||||||||  
 Qy 563 TQSQDLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGSPSPHSELVWDVAEANRSQVK 622  
 Db |||||||||  
 Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIMGDVHRLMTATQYVAPLMA 180  
 Db |||||||||  
 Qy 623 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIMGDVHRLMTATQYVAPLMA 682  
 Db |||||||||  
 Qy 181 NFNPYSDNSTVYFDNGTVFVQMDHVYLGQWEDKGSFTFOAALHHDGRIVFYAKEIPM 240  
 Db |||||||||  
 Qy 683 NFNPYSDNSTVYFDNGTVFVQMDHVYLGQWEDKGSFTFOAALHHDGRIVFYAKEIPM 742  
 Db |||||||||  
 Qy 241 SVPEISSQHPVKTKGLSDFAMILNPSPDVPSRRRSIFEVHRIELDPKVTSMASVEFTP 802  
 Db |||||||||  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDFQ 360  
 Db |||||||||  
 Qy 803 LPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDFQ 862  
 Db |||||||||  
 Qy 361 DEDHDSAPDTSFSPYDGLTTSSSLFIDSLTTFEDDTKLPYAGGDLQNNLSPKTKGT 420  
 Db |||||||||  
 Qy 863 DEDHDSAPDTSFSPYDGLTTSSSLFIDSLTTFEDDTKLPYAGGDLQNNLSPKTKGT 922  
 Db |||||||||  
 Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHST 480  
 Db |||||||||  
 Qy 923 PVHLGTIVGIVLAVLLVAAILAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHST 982  
 Db |||||||||  
 Qy 481 YAEVPSGHEKEGFMEARQC 500  
 Db |||||||||  
 Qy 983 YAEVPSGHEKEGFMEARQC 1002  
 Db |||||||||  
 RESULT 8  
 ABUS4430  
 ID ABUS44430 standard; protein; 1002 AA.  
 XX  
 AC ABUS44430;

XX 12-MAR-2003 (first entry)  
 XX Human tumour endothelial marker TEM 8.  
 DE  
 XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
 XX Tumour endothelial marker; normal endothelial marker; PEM;  
 XX pan-endothelial marker; polycystic kidney disease; psoriasis;  
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
 KW neoangiogenesis; immune response; cytostatic; antidiabetic;  
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200283874-A2.  
 XX  
 XX 24-OCT-2002.  
 PD  
 XX 10-APR-2002; 2002WO-US008253.  
 PF  
 XX 11-APR-2001; 2001US-0282850P.  
 PR  
 XX 06-FEB-2002; 2002US-0354262P.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
 PI  
 XX WPI; 2003-093016/08.  
 DR  
 XX N-PSDB; ABX72003.  
 DR  
 XX New purified human transmembrane protein, designated as tumor endothelial  
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
 PT psoriasis.  
 XX  
 XX Disclosure; Page 122-124; 374pp; English.  
 PS  
 XX The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. The present  
 CC sequence represents a human TEM or NEM protein of the invention  
 XX  
 SQ Sequence 1002 AA;  
 Query Match 100.0%; Score 2691; DB 6; Length 1002;  
 Best Local Similarity 100.0%; Pred. No. 9e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRGELLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 60  
 Db |||||||||  
 Qy 503 MRGELLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRARSPGHVSPDR 562  
 Db |||||||||  
 Qy 61 TQSQDLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGSPSPHSELVWDVAEANRSQVK 120  
 Db |||||||||  
 Qy 563 TQSQDLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGSPSPHSELVWDVAEANRSQVK 622  
 Db |||||||||  
 Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIMGDVHRLMTATQYVAPLMA 180  
 Db |||||||||  
 Qy 623 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIMGDVHRLMTATQYVAPLMA 682  
 Db |||||||||  
 Qy 181 NFNPYSDNSTVYFDNGTVFVQMDHVYLGQWEDKGSFTFOAALHHDGRIVFYAKEIPM 240  
 Db |||||||||  
 Qy 683 NFNPYSDNSTVYFDNGTVFVQMDHVYLGQWEDKGSFTFOAALHHDGRIVFYAKEIPM 742  
 Db |||||||||  
 Qy 241 SVPEISSQHPVKTKGLSDFAMILNPSPDVPSRRRSIFEVHRIELDPKVTSMASVEFTP 300

Db 743 SVPEISSQHPVKTLGSLDAFNLNPSDPVPSRRSIFEHRIELDPKSVTMSAVEFTP 802  
 Qy 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 360  
 Db 803 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 862  
 Qy 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420  
 Db 863 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 922  
 Qy 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480  
 Db 923 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982  
 Qy 481 YAEVEPSGHEKEGFMEAEQC 500  
 Db 983 YAEVEPSGHEKEGFMEAEQC 1002

## RESULT 9

ADI21064  
 ID ADI21064 standard; protein; 488 AA.

AC ADI21064;

XX 15-APR-2004 (first entry)

XX Novel human protein #39.

XX forensic; nutritional source; damaged tissue; disease tissue;  
 KW myeloid cell disorder; lymphoid cell disorder;  
 KW bone cartilage tissue growth; tendon tissue growth;  
 KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;  
 KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

XX Homo sapiens.

XX WO2003025148-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-US029964.

XX 19-SEP-2001; 2001US-0323739P.

XX 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;  
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;  
 PI Haley-Vicente D;

DR WPI; 2003-354603/33.

DR N-PSDB; ADI21780.

XX New polynucleotides and secreted proteins, useful for treating myeloid or  
 PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve  
 PT tissue growth or regeneration, in wound healing, and in tissue repair and  
 PT replacement.

XX Claim 20; SEQ ID NO 315; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a  
 CC polypeptide with biological activity. The polynucleotides and  
 CC polypeptides are useful in diagnostics, forensics, gene mapping,  
 CC identification of mutations responsible for genetic disorders and other  
 CC traits, to assess biodiversity, as nutritional sources or supplements.  
 CC The polynucleotides may also be used as molecular weight markers,  
 CC chromosome markers or map related gene positions, or as an antigen to  
 CC raise anti-DNA antibodies or elicit immune response. The polypeptides are  
 CC useful for raising antibodies, as markers for tissues in which the  
 CC corresponding polypeptide is expressed, for re-engineering damaged or

CC diseased tissues, for treating myeloid or lymphoid cell disorders, in  
 CC bone cartilage, tendon, ligament and/or nerve tissue growth or  
 CC regeneration, in wound healing, in tissue repair and replacement, in  
 CC healing of burns, incisions and ulcers, and in treating cancer. The  
 CC present sequence represents the amino acid sequence of a novel human  
 CC protein.

XX SQ Sequence 488 AA;

Query Match 96.9%; Score 2607; DB 7; Length 488;

Best Local Similarity 97.6%; Pred. No. 3.5e-241;

Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEDPDR 60

Db 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEDPDR 60

Qy 61 TQLSQDLGGGTFLAMDTLPDNRTRVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120

Db 61 TQLSQDLGGGTFLAMDTLPDNRTRVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120

Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIFMGDVITHRLMTATQYVAPLMA 180

Db 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITATGGFIFMGDVITHRLMTATQYVAPLMA 180

Qy 181 NFNEGYSDNSTVYFDNGTVFVQMDHYVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Db 181 NFNEGYSDNSTVYFDNGTVFVQMDHYVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTLGSLDAFNLNPSDPVPSRRSIFEHRIELDPKSVTMSAVEFTP 300

Db 241 SVPEISSQHPVKTLGSLDAFNLNPSDPVPSRRSIFEHRIELDPKSVTMSAVEFTP 300

Qy 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 360

Db 301 LPTCLQHRSCDACMSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 360

Qy 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420

Db 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420

Qy 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480

Db 409 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 468

Qy 481 YAEVEPSGHEKEGFMEAEQC 500

Db 469 YAEVEPSGHEKEGFMEAEQC 488

## RESULT 10

ABB90783

ID ABB90783 standard; protein; 500 AA.

XX AC ABB90783;

XX 30-MAY-2002 (first entry)

XX Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis.

XX Mus musculus.

XX WO200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US024031.

XX 02-AUG-2000; 2000US-0222599P.  
PR 11-AUG-2000; 2000US-0224360P.  
PR 11-APR-2001; 2001US-0282850P.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX St Croix B, Kinzler KW, Vogelstein B;  
XX WPI; 2002-291856/33.  
DR N-PSDB; ABL92136.  
XX An isolated molecule comprising an antibody variable region which  
PT specifically binds to an extracellular domain of a tumor endothelial  
PT marker (TEM) protein, useful for inhibiting tumor growth.  
XX  
XX  
PS Disclosure; Page 301-302; 331pp; English.  
XX  
XX The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumor growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995  
XX  
SQ Sequence 500 AA;  
  
Query Match 82.1%; Score 2209; DB 5; Length 500;  
Best Local Similarity 81.6%; Pred. No. 6.7e-203;  
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;  
  
Qy 1 MRGELWLL-VLVAREAAALSPQAGHDEGPGSGWAAKGTGVRGNRRARSPGHVSEPD 59  
Db 1 MRAQLWLLQLLLKGAARALSPATPAGHNEQDQSAWTAKTTRQGSRRPRSPAQLKPG 60  
  
Qy 60 RTQLSQDLGGGTGLAMDTLPDNRTRVEDNHNHYSRLYSPSEPHSRLWVDVAENRSQV 119  
Db 61 KTQLSQDLGGGSLAIDLTPDNRTRVEDNHNHYSRVYVPGCEKQSDLLWDLVANRSHV 120  
  
Qy 120 KIHTILSNTHROASRVLSFDPPFYGHPLRQITATTGCFIPMGDVIIHRMLTATQYVAPLM 179  
Db 121 KIHRISSSHRQASRVLSFDPPFYGHPLRQITATTGCFIPMGDMLHRMLTATQYVAPLM 180  
  
Qy 180 ANENPGYSDNVTYVFDNGTVVQWHDVYLOQWEDKGSFTFOALHHDGRIVFAYKEIP 239  
Db 181 ANENPGYSDNVTYVFDNGTVVQWHDVYLOQWEDKGSFTFOALHHDGRIVFAYKEIP 240  
  
Qy 240 MSVPEISSQHPVKTGLSDAFMLNPSDPVPESSRRRSIFFYHRIELDPSKVTMSAVEFT 299  
Db 241 MAVLDISSAQHPVKAAGLSDAFMLNPSPEVPESSQRTTFEYHRLVDELSSKITTSAVEFT 300  
  
Qy 300 PLPTCLQRSQDACHMSDLTNCNCHVLRQCSGFDRIYRQEWMDYCAQAEGRMCEDF 359  
Db 301 PLPTCLQHQSCDTCVSSNLTFNCNCHVLRQCSGFDRIYRQEWMDYCAQAEGRMCEDF 360  
  
Qy 360 QDEHDSASPTSPYDGLTTTTSSSLFIDSLTDEDTKLNPNYAGDGLONNLSPTK 419  
Db 361 QDDSHYSASPOSSFPFNGD-STTSSSLFIDSLTDEDTKLNPNYAGDGLPDHSPSKG 419  
  
Qy 420 TPVHLGTIVGIVLVAIIAGIYINGHPTNSAALFFIERRPHWPAMKFRSHPDHS 479  
Db 420 PPVHLGTIVGIVLVAIIAGIYISGHPNSNAALFFIERRPHWPAMKFRSHPDHS 479  
  
Qy 480 TYAEVPSGHEKEGFMAEQ 500  
Db 480 TYTEVPSGHEKEGFMVEQ 500

RESULT 11

ABB90729 standard; protein; 500 AA.

ABB90729;

30-MAY-2002 (first entry)

Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.

Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
normal endothelial marker; pan-endothelial marker; immunostimulant;  
antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
psoriasis.

Mus musculus.

WO200210217-A2.

07-FEB-2002.

01-AUG-2001; 2001WO-US024031.

02-AUG-2000; 2000US-0222599P.

11-AUG-2000; 2000US-0224360P.

11-APR-2001; 2001US-0282850P.

(UYJO ) UNIV JOHNS HOPKINS.

St Croix B, Kinzler KW, Vogelstein B;

WPI; 2002-291856/33.

An isolated molecule comprising an antibody variable region which  
specifically binds to an extracellular domain of a tumor endothelial  
marker (TEM) protein, useful for inhibiting tumor growth.

Disclosure; Page 146-147; 331pp; English.

The invention relates to an isolated molecule comprising an antibody  
variable region which specifically binds to an extracellular domain of a  
tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
proteins have cytostatic, immunostimulant and antiangiogenic activity.  
They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
bearing a vascularised tumour, polycystic kidney disease, diabetic  
retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
are disclosed, as are marker oligonucleotide sequences: tumour  
endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
(PEM) ABL91903-ABL91995

Sequence 500 AA;

Query Match 82.1%; Score 2209; DB 5; Length 500;

Best Local Similarity 81.6%; Pred. No. 6.7e-203;

Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

1 MRGELWLL-VLVAREAAALSPQAGHDEGPGSGWAAKGTGVRGNRRARSPGHVSEPD 59

1 MRAQLWLLQLLLKGAARALSPATPAGHNEQDQSAWTAKTTRQGSRRPRSPAQLKPG 60

60 RTQLSQDLGGGTGLAMDTLPDNRTRVEDNHNHYSRLYSPSEPHSRLWVDVAENRSQV 119

61 KTQLSQDLGGGSLAIDLTPDNRTRVEDNHNHYSRVYVPGCEKQSDLLWDLVANRSHV 120

120 KIHTILSNTHROASRVLSFDPPFYGHPLRQITATTGCFIPMGDVIIHRMLTATQYVAPLM 179

121 KIHRISSSHRQASRVLSFDPPFYGHPLRQITATTGCFIPMGDMLHRMLTATQYVAPLM 180





Db 121 VYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180  
 Qy 252 VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASAVEFTPLTCLQHRSCD 311  
 Db 181 VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASAVEFTPLTCLQHRSCD 240  
 Qy 312 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----ED 363  
 Db 241 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----QDVRGLPGMRT 294  
 Qy 364 HDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVH 423  
 Db 295 TTSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVH 354  
 Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 483  
 Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 414  
 Qy 484 VEPGHEKEGFMABEQ 500  
 Db 415 VEPGHEKEGFMABEQ 431

## RESULT 15

AB001434  
 ID AB001434 standard; protein; 431 AA.

XX AC AB001434;

DT 07-AUG-2003 (first entry)

XX DE Human tumour endothelial marker 7 precursor protein.

XX KW Human; Gene therapy; stem cell inducer; osteoporosis; regeneration;  
 KW stem cell growth factor-like activity; leukaemia; haemophilia; allergy;  
 KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;  
 KW autoimmune disease; multiple sclerosis; systemic lupus erythematosus;  
 KW graft-versus-host disease; degenerative disease; Alzheimer's disease;  
 KW osteoarthritis; anaemia; tendonitis; carpal tunnel syndrome; cancer;  
 KW tumour endothelial marker 7 precursor.

XX OS Homo sapiens.

XX PN US2003022825-A1.

XX PD 30-JAN-2003.

XX PF 24-JUL-2001; 2001US-00912935.

XX PR 23-DEC-2000; 2000WO-US035260.

XX PA (NISHI/) NISHIKAWA M.

XX PA (LABA/) LABAT I.

XX PA (DRMA/) DRMANAC R T.

XX PA (TANG/) TANG Y T.

XX PA (CHAO/) CHAO C.

XX PI Nishikawa M, Labat I, Drmanac RT, Tang YT, Chao C;

XX DR WPI; 2003-456302/43.

XX PT New stem cell growth factor-like polypeptides and polynucleotides, useful  
 for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis,  
 PT graft-versus-host disease, cancers, Alzheimer's disease, Huntington's  
 PT disease.

XX PS Example 4; Fig 2; 98pp; English.

XX CC The invention relates to a new isolated polypeptide, which has stem cell  
 growth factor-like activity. The new polypeptide, the polynucleotide  
 CC encoding this polypeptide, or the agonist of the polypeptide are useful  
 CC for treating a subject in need of enhanced activity or expression of stem  
 CC cell growth factor-like polypeptide. The antagonist of the polypeptide or

CC the polynucleotide is useful for treating a subject in need to inhibit  
 CC the activity or expression of stem cell growth factor-like polypeptide.  
 CC The new polypeptide or polynucleotide is particularly useful for inducing  
 CC differentiation of embryonic and adult stem cells to give rise to  
 CC different cell types. In particular, the polypeptide or polynucleotide is  
 CC useful for treating leukaemia, haemophilia, osteoporosis, osteoarthritis,  
 CC anaemia, tendonitis, carpal tunnel syndrome, autoimmune diseases (e.g.  
 CC multiple sclerosis, systemic lupus erythematosus, graft-versus-host  
 CC disease or allergies), cancers or degenerative diseases (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease or amyotrophic lateral  
 CC sclerosis) or for generating new tissues and organs that may aid patients  
 CC in need of transplanted tissues. The polynucleotide may also be used in  
 CC gene therapy for the treatment of these diseases. The new polypeptide or  
 CC polynucleotide is also useful in diagnostic or research methods. The  
 CC present sequence represents the human tumour endothelial marker 7  
 CC precursor protein

XX SQ Sequence 431 AA;

Query Match 81.2%; Score 2185; DB 6; Length 431;  
 Best Local Similarity 95.2%; Pred. No. 1.1e-200;  
 Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 72 LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHSRELWVDVAENRSQVKHTILSNTHRQ 131  
 Db 1 LAMDTLPDNRTRVVEDNHSYVSRLYGSPSPHSRELWVDVAENRSQVKHTILSNTHRQ 60  
 Qy 132 ASRVLSDFDPFFYGHPLRQITATGGFIFMGDVTHRMLTATQYVAPLMANFNPGYSDNST 191  
 Db 61 ASRVLSDFDPFFYGHPLRQITATGGFIFMGDVTHRMLTATQYVAPLMANFNPGYSDNST 120  
 Qy 192 VVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 251  
 Db 121 VVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180  
 Qy 252 VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASAVEFTPLTCLQHRSCD 311  
 Db 181 VKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTSMASAVEFTPLTCLQHRSCD 240  
 Qy 312 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----ED 363  
 Db 241 ACMSSDLTFNCWCHVLQRCSSGDFDRYQEW-MDYGCAQAEGRMCEDFQD-----QDVRGLPGMRT 294  
 Qy 364 HDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVH 423  
 Db 295 TTSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGTPVH 354  
 Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 483  
 Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHWPAMKFRSHPDHSTYAE 414  
 Qy 484 VEPGHEKEGFMABEQ 500  
 Db 415 VEPGHEKEGFMABEQ 431

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 Job time : 160.818 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Perfect score: 370

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	488	17	US-10-357-819-4
2	370	100.0	500	10	US-09-918-715-230
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4	370	100.0	500	17	US-10-474-794-230
5	370	100.0	500	17	US-10-357-819-2
6	370	100.0	1002	10	US-09-918-715-179
7	370	100.0	1002	17	US-10-474-794-179
8	359	97.0	431	14	US-09-912-935-36
9	359	97.0	431	14	US-10-168-365-36
10	359	97.0	502	14	US-10-156-487A-5
11	325	87.8	500	10	US-09-918-715-192
12	325	87.8	500	10	US-09-918-715-297
13	325	87.8	500	14	US-10-156-487A-6

14	325	87.8	500	17	US-10-474-794-192
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17	264	71.4	530	10	US-09-918-715-299
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19	264	71.4	530	14	US-10-156-487A-2
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28	263	71.1	425	14	US-09-912-935-35
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33	263	71.1	499	14	US-10-168-365-31
34	263	71.1	529	10	US-09-918-715-189
35	263	71.1	529	10	US-09-918-715-200
36	263	71.1	529	10	US-09-912-935-28
37	263	71.1	529	10	US-09-912-935-40
38	263	71.1	529	13	US-10-052-586-472
39	263	71.1	529	13	US-10-066-500-128
40	263	71.1	529	14	US-10-174-590-472
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ALIGNMENTS

RESULT 1  
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; Publication No. US20040259774A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Li, Li  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Sytek, Kimberly A.  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-538A  
; CURRENT APPLICATION NUMBER: US/10/357,819  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: 09/520,781  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 09/584,411  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 09/783,436  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 10/085,198  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/353,301

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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
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Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60
   |||||
Db 280 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 339

Qy 61 QEWMD 65
   |||||
Db 340 QEWMD 344
```

RESULT 2

```
US-09-918-715-230
; Sequence 230, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-230
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Query Match      100.0%; Score 370; DB 10; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60
   |||||
Db 280 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 339

Qy 61 QEWMD 65
   |||||
Db 340 QEWMD 344
```

RESULT 3

```
US-10-435-696-79
; Sequence 79, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-79
```

```
Query Match      100.0%; Score 370; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60
   |||||
Db 280 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 339

Qy 61 QEWMD 65
   |||||
Db 340 QEWMD 344
```

RESULT 4

```
US-10-474-794-230
; Sequence 230, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-230
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```
Query Match      100.0%; Score 370; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60
   |||||
Db 280 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 339

Qy 61 QEWMD 65
   |||||
Db 340 QEWMD 344
```

```
RESULT 5
US-10-357-819-2
; Sequence 2, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,367
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-819-2

Query Match      100.0%; Score 370; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGGFDRYR 60
Db 280 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGGFDRYR 339
Qy 61 QEWMD 65
Db 340 QEWMD 344

RESULT 6
US-09-918-715-179
```

```
; Sequence 179, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179

Query Match      100.0%; Score 370; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGGFDRYR 60
Db 782 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGGFDRYR 841
Qy 61 QEWMD 65
Db 842 QEWMD 846

RESULT 7
US-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-179

Query Match      100.0%; Score 370; DB 17; Length 1002;
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGGFDRYR 60
Db 782 YHRIELDPKVTSMASVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGGFDRYR 841
Qy 61 QEWMD 65
Db 842 QEWMD 846
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```
RESULT 8
US-09-912-935-36
; Sequence 36, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-36

Query Match          97.0%; Score 359; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 209 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 268

Qy 61 QEW 63
Db 269 QEW 271

RESULT 9
US-10-168-365-36
; Sequence 36, Application US/10168365
; Publication No. US20030211987A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Childs, John
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Mize, Nancy
; APPLICANT: Lee, Juh1
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 30266/37630
; CURRENT APPLICATION NUMBER: US/10/168,365
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-365-36

Query Match          97.0%; Score 359; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 209 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 268

Qy 61 QEW 63
Db 269 QEW 271

RESULT 10
US-10-156-487A-5
; Sequence 5, Application US/10156487A
; Publication No. US20030092025A1
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match          97.0%; Score 359; DB 14; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 280 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 339

Qy 61 QEW 63
Db 340 QEW 342

RESULT 11
US-09-918-715-192
; Sequence 192, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-192

Query Match          87.8%; Score 325; DB 10; Length 500;
Best Local Similarity 84.4%; Pred. No. 5.7e-31;
Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 281 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 340

Qy 61 QEW 64
Db 340 QEW 342
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RESULT 8
US-09-912-935-36
; Sequence 36, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-36

Query Match          97.0%; Score 359; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 209 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 268

Qy 61 QEW 63
Db 269 QEW 271

RESULT 9
US-10-168-365-36
; Sequence 36, Application US/10168365
; Publication No. US20030211987A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Childs, John
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Mize, Nancy
; APPLICANT: Lee, Juh1
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 30266/37630
; CURRENT APPLICATION NUMBER: US/10/168,365
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-365-36

Query Match          97.0%; Score 359; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 209 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 268

Qy 61 QEW 63
Db 269 QEW 271

RESULT 10
US-10-156-487A-5
; Sequence 5, Application US/10156487A
; Publication No. US20030092025A1
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match          97.0%; Score 359; DB 14; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 280 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 339

Qy 61 QEW 63
Db 340 QEW 342

RESULT 11
US-09-918-715-192
; Sequence 192, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-192

Query Match          87.8%; Score 325; DB 10; Length 500;
Best Local Similarity 84.4%; Pred. No. 5.7e-31;
Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 60
Db 281 YHRIELDPKVTSMASAVEFTPLPTCLOHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYR 340

Qy 61 QEW 64
Db 340 QEW 342
```

Qy 1 YHIELDPSKVTMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYR 60

Db 281 YHRVELDSSKITTTSAVEFTPLPTCLQHQSCDTCVSSNLTFNC5WCHVQRCSSGFDYR 340

Qy 61 QEW 64

Db 341 QEW 344

Search completed: January 28, 2005, 22:19:19  
Job time : 18.7655 secs







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Db 180 SPADTPPTSAITMHPASVODQTTVRTVASAATANEIRQSSSYEDPW-----KITDE- 232
Qy 139 GGFIFMGDVHRLMTATQY--VAPLMANFNPGYSDNSTVVYFDNGTVFVQWMDHVV-LQG 195
Db 233 -----QRYVNVQFKTIQDLNGFIQF---SAAKEFTYKSKPILELSHWELSD 279
Qy 196 WEDKGSFT---FOAALHHDGRIVFAYK---BIPMSVPEISSQHPVKTGLSDAFMILNPS 249
Db 280 FDKDGAULTDFECAAFFH---LVARKNGYDLPEKLP-----SLMPKLIDLEDS 325
Qy 250 PDVPESSRRRSIFEYHRIELDPKSKYTSMSAVEFTPLPTCLOHRSQCDACMSSDLTNCWSCH 309
Db 326 ADVGEQFGEVGYSGPAEAPPSPSPSL-----NOTWPE 361
Qy 310 VLQRCSSGFDYRQEWMDYGAQBAEGRMCDFOEDHDSASPOTS----- 355
Db 362 LNQS-----SEQWETFS-ERSSSQTLTQF-DSNIAPADPTAIVHPVPIRMTPSKI 411
Qy 356 -----FSPYDGLTTSSTSSLFIDSLTTEDTKLNP-----YAGDGLQNNLS 397
Db 412 HMQEMELKRTSSDHTNPTSPVLKPSDLSEENKINSSVKPPSGNTVDGYSSSDSPSPD-- 469
Qy 398 PKTKGTPV-----HLGT 409
Db 470 PEQIGSSVTRQSRHSGT 486

RESULT 5
C86446
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86446
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-979 <STO>
A;Cross-references: UNIPROT:Q9FVR3; GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G
C;Genetics:
A;Map position: 1

Query Match 4.5%; Score 100.5; DB 2; Length 979;
Best Local Similarity 21.1%; Pred. No. 6.1;
Matches 83; Conservative 47; Mismatches 155; Indels 109; Gaps 19;

Qy 4 POPGAGHDEGPGCGAAKGTVRGNRRARESPGHVSEPDRTQLSQDL-----G 51
Db 359 PRPAL-----VAPKATWMSDGT--HWPGTWAVSGPHHSGRGRDHSASVIQVLLDPPGDPVGVGK 413
Qy 52 GGTLLMD-----TLPDNRTRVVDNHSYVYRLYGPSPHRSRELDVDAEANSQVKIH 105
Db 414 GEGRALDLEGVDIRLP-----MLVYVSRKRPYDHNKK-----AGANNALVRAS 458
Qy 106 TILSNTHQASRVVLSDFEPYGHPLRQITATGGTIFMGDVHRLMTATQY----- 157
Db 459 AIMSND-----GPFILNLDCHYVNSRAF---RDGICFMMDHGDGRVSYVQFPORFEGID 510
Qy 158 VAPLMANFNPGYSD-----NSTVYV-FDNGTVFVQWMDHVVLOG 195
Db 511 PSDRYANKNTVFFDINLRALDGIQGMVYGTGCLFRRTALYGFNPDPVFWVE----- 562
```

```
Qy 196 WEDKGSFTFOAALHHDGRIVFAYKEIPMSV---PEISSQHP-----VKTGLSDAFMIL 246
Db 563 EEPGSGYCFP-----LIKRSPTAVASEEYTYTDEEDRFDIGLIRKQFGSSSMLV 612
Qy 247 NPSPDVPESRRRSIFEVH--RIELDPKSKVT--SMSAVEFTPLPTCLOHRSQCDACMSSDLTF 303
Db 613 N-SVKVAEFGEPRLATVHSSRLGPPGSLTGSRLKPLDFATVNEAVNVIWCYEDKTEWGF 671
Qy 304 NCSCCH--VLQRCSSGFDYRQEWMDYGAQBAE 335
Db 672 NVGMIYGSVTEVDVYTFGRMEKGRSFYCVTEPD 705

RESULT 6
S18606
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.
C;Species: Rhizobium sp.
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003
C;Accession: S18606
R;Osteras, M.; Finan, T.M.; Stanley, J.
Mol. Gen. Genet. 230, 257-269, 1991
A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encodin
A;Reference number: S18606; MUID:92079905; PMID:1720862
A;Accession: S18606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <OST>
A;Cross-references: EMBL:X63291
C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop
F;234-241/Region: nucleotide-binding motif A (P-loop)

Query Match 4.5%; Score 99; DB 2; Length 535;
Best Local Similarity 20.7%; Pred. No. 3.5;
Matches 59; Conservative 39; Mismatches 117; Indels 70; Gaps 12;

Qy 61 PDNRTRVVD-----NHSYVSRLYGPSPHRSRELDVDAEANSQVKIHTI-LSNTHR 113
Db 86 PENFERLRQDLAHAKGMSLYQDLVGAGSGK-----CVADARRHRIRHWSLSLFTIRLLI 140
Qy 114 QASRVVLS-----PDFP-FYGHF-----LRQITATGGFIFMGDVHVR 150
Db 141 RPPREGLASFLPKLTITIDLSPFKANPERHGCGRGTIIACDLTKGLVLIGGTSYAGEMKKS 200
Qy 151 MLTATQTVAP-----LMANFNPGYSDNSTVYF-----DNGTVFVQWMDH 190
Db 201 VFTVNLVLLPNKAVPMHCSANVCPA---GDTAIFFGLSGTGKTLSDPNRTLIGDDEH 257
Qy 191 VYLGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPS 250
Db 258 ----GMSDKGVFNPEG-----GCYAKAIRLSEAAEPFIFATRRFRFGTMENVVLDERRAP 308
Qy 251 DVPESSRRRSIFEYHRIELDPKSKYTSMSAVEFTPLPTCLOHRSQCD 295
Db 309 DFONG-----SLTENTRIAYPLDFIPNASETGTAPOQFRTIIMLTADA 350

RESULT 7
T12529
hypothetical protein DKFZp434p13.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12529
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
A;Accession: T12529
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1133 <WAM>
A;Cross-references: UNIPROT:Q9UG37; EMBL:AL080145
A;Experimental source: adult testis; clone DKFZp434p13
C;Genetics:
```

A;Note: DKFZp434P113.1

```
Query Match          4.5%; Score 99; DB 2; Length 1133;
Best Local Similarity 23.0%; Pred. No. 10;
Matches 67; Conservative 37; Mismatches 119; Indels 68; Gaps 16;

Qy 145 GDVHRLMTAQYVAPLMAFNPVGSNSTVYVFDNGTVFVQVMDHVVYVLOG--WE----- 197
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 823 GDIAH--IYDIQTGNKLLTLPNPLANN-----YKENCATFNPTDLDVLNDGVLDVRSQA 876

Qy 198 -----DKGSFTTQALHHHGRIVFAYKEI-----PMSVPEISSSQ---HPVKTLGSD 241
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 877 AIHKFDKFNMMNISGVFHPNGLEVIINTEIMDLRTFHLHLHTVPALDQCRVVENHTGTVMYG 936

Qy 242 AFMLNPSPPVPESSRRSIFEHYRIELDPKSVTSMSAVFPLPTC-LQHRSCDACWSSD 300
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 937 AMLOADEDDELMERMKSPF-----GSSFRFNATDYKPIATIDYKRNIFPLCTD-- 986

Qy 301 LTFNCSCWHLQRCSSGFDYRQEWMDYGC-----AQEAEGRMCEDFQEDDH 347
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 987 -TKDC-YLAVIENQGS-WDALN---MDTVCLRYEVRQRLAEDDEDEDEQEEQEEDEDD 1040

Qy 348 DSASPDTSFSPYDGLTTTSSSLFIDSLTBDDTKLNPYAGDGLQNNLSP 398
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1041 DEDDDTD-----DLDELTDQLLEALELEDDN--NENAGEDG-DNDFSP 1082
```

#### RESULT 8

```
S45429
probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBL0725
C;Species: Saccharomyces cerevisiae
C;Date: 09-Jun-1994 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S45429; S45820; S45815; S59226
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A;Description: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevisiae chromosome 1.
A;Reference number: S45387
A;Accession: S45429
A;Molecule type: DNA
A;Residues: 1-1502 <OBE>
A;Cross-references: UNIPROT:P38181; EMBL:X79489; NID:G496661; PID:G496702
A;Experimental source: strain S288C
R;Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45816
A;Accession: S45820
A;Molecule type: DNA
A;Residues: 1-1502 <DOM>
A;Cross-references: EMBL:X35840; NID:G536126; PID:G536127; MIPS:YBL079w
A;Experimental source: strain S288C
R;Contreras, R.; Fiers, W.; Logghe, M.; Molenans, F.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45802
A;Accession: S45815
A;Molecule type: DNA
A;Residues: 1262-1502 <CON>
A;Cross-references: EMBL:X35840; MIPS:YBL079w
A;Experimental source: strain S288C
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
Yeast 11, 1103-1112, 1995
A;Title: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevisiae chromosome 1.
A;Reference number: S59184; MUID:96076635; PMID:7502586
A;Accession: S59226
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1502 <OBW>
A;Cross-references: EMBL:X79489; NID:G496661; PID:CAA56029.1; PID:G496702
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C;Genetics:
A;Gene: SGD:NUP170
A;Cross-references: SGD:S0000175; MIPS:YBL079w
A;Map position: 2L
```

C;Keywords: nucleus; transmembrane protein  
F;231-247/Domain: transmembrane #status predicted <TM1>  
F;434-450/Domain: transmembrane #status predicted <TM2>  
F;764-780/Domain: transmembrane #status predicted <TM3>  
F;1311-1327/Domain: transmembrane #status predicted <TM4>  
F;1382-1399/Domain: transmembrane #status predicted <TM5>  
F;1406-1423/Domain: transmembrane #status predicted <TM6>

Query Match 4.4%; Score 98; DB 2; Length 1502;

```
Best Local Similarity 22.7%; Pred. No. 18;
Matches 62; Conservative 41; Mismatches 106; Indels 64; Gaps 14;

Qy 44 TQLSQDLGGGTGLAMDTLPDNRTRVVDNHSYVYVSRLYGCPSEPHSRRLWVDVAEANSQVK 103
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 778 TRLRLDIWGRVFM-TFTDNRV---TSHAFISS--DPITPSINNLKSDAISQNRNII- 829

Qy 104 IHTILSNTHROAGRWVLSFD-PPFYGHPLRQITATGGIFPMGDIHRLMTATQYVAP-L 161
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 830 -----SKVSISKDCIEYY--LSSINILNEFFITYGDSI-----SQISAPYV 868

Qy 162 MANENPGYSNISTVYVFD-----NGTVFVQVMDHVVYVLOGWEDKGSFTTQALHHHGR 214
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 869 LANNNGSRVIDKTEEVANQAESAINAMIKVQ-----SIKEGLSFLNLVYSESV 919

Qy 215 -----VFAYKEIPMSVPEISSSQHPVKTKGLSDAFMLNPSDPVPESSRRSIFEHYRIEL 268
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 920 EGFNDQVILGFKDI-ISFVSLDVQKDLVLPDKLDF-----APNDKTKSLIREILLSI 970

Qy 269 DPSKVTMSAVETPLPTCLOHRSCDACMSSDL 301
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 971 INRNITKGASIEVT--ATALQERCSPCSASDI 1001
```

#### RESULT 9

```
S33415
corticosteroid-binding globulin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S33415; S43740
R;Srocchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L.
Endocrinology 132, 903-909, 1993
A;Title: Spatial and temporal distribution of corticosteroid-binding globulin and its mRNA
A;Reference number: S33415; MUID:93145908; PMID:7916682
A;Accession: S33415
A;Molecule type: mRNA
A;Residues: 1-397 <SCR1>
A;Cross-references: UNIPROT:Q06770; EMBL:X70533; NID:G298114; PID:CAA49934.1; PID:G2981
A;Accession: S43740
A;Molecule type: protein
A;Residues: 23-40 <SCR2>
C;Superfamily: Serpin
C;Keywords: Glycoprotein; steroid binding
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-397/Product: corticosteroid-binding globulin #status experimental <MAT>
F;89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

Query Match 4.4%; Score 96.5; DB 2; Length 397;

```
Best Local Similarity 20.2%; Pred. No. 3.8;
Matches 53; Conservative 47; Mismatches 104; Indels 59; Gaps 11;

Qy 44 TQLSQDLGGGTGLAMDTLPDNRTRVVDNHSYVYVSRLYGCPSEPHSRRLWVDVAE-----A 97
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 114 TGLEMNGVWFLQNLKLDKSLADTKHYESENALTIPTSKD-----WTRAGEQINNHNK 168

Qy 98 NRSQVKIHTILSNTHROASRWVLSFD-----PFYGHPLRQITATGGIFPMGDIHRL 150
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 169 NKTQGGKIEHVVDLSSATLILINIFLKGWLKLPFPSPENTRE-----EDFYV 216

Qy 151 MLTATQVVAIPLMANFNPGYSNISTV-----YFDNGTVFVQVMDHVVYVLOGWEDKGSFT 203
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 217 NETSTVKVPMVQSGNISYFRDSPAICQMVMQMVNGTTFIILPD-----QGQMD-----T 268

Qy 204 FQALHHD-----GRIVFAYKEIPMSVPEISSSQH-----PVKTGLSDAFMLNPSDPV 252
```

```
Db 269 VVAALNEDTIDRWGKMLIP-RQMLYIPKFSMSDTYLDQVLADVGIKDLFTNOSDFADT 327
Qy 253 PESRRRSIFEYHR--IELDPSKV 273
Db 328 TKDTPFLITLVHLKAMQLDEGNV 350

RESULT 10
T19703
hypothetical protein C34C12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19703
R;Kerhaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19166
A;Accession: T19703
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-679 <WIL>
A;Cross-references: UNIPROT:Q09495; EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GN00021; CESP:C3
A;Experimental source: clone C34C12
C;Genetics:
A;Gene: CESP:C34C12.2
A;Map position: 3
A;Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3

Query Match 4.3%; Score 95.5; DB 2; Length 679;
Best Local Similarity 24.4%; Pred. No. 9.6; Mismatches 31; Indels 65; Gaps 12;
Matches 65; Conservative 31;

Qy 34 SPGHVSFDPDTQLSDLGSGTGLAMDTLPDNRTRVVDNHSYVGRLYGSPSPHRELWVD 93
Db 372 SPG---PPGRQISDLQNTGEVRY-----VNSSGKPFNS-----SESNSRLKLI 414

Qy 94 VAEANRSQ---VKHTILSNTHRQASRVLSFDPPFGHPLRQITAT-----GGFIM 144
Db 415 PGYIKRPEFRYKPEGTSTASYKAQSGMSF-----LKTGSSATPENSCKSAHFDM 466

Qy 145 GDVTHMLTATQYVAPLMAANNPGYSDNSTVVF-----DNGTVFVQWDHVLQGWEDK 199
Db 467 PDI-----SSTPYKSHVVVSDEMNSSSTIGGFESKKGNGAL-----GSQKS 510

Qy 200 GSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRS 259
Db 511 PMPDIATALHN----IFDSKEVQSSSTTGSAPENSKSDHF-----DMPDISSTLYRS 562

Qy 260 IFYVHRIELDPKVTSMASAVEFTPLP 285
Db 563 RVE--PISSSSSGSTSTSAPIYVKP 586

RESULT 11
T30243
alpha tectorin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30243
R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
Hear. Res. 130, 62-74, 1999
A;Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.
A;Reference number: Z20783; MUID:99251817; PMID:10320099
A;Accession: T30243
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2120 <COU>
A;Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:e1361091; PIDN:CAAC
A;Note: non-collagenous protein only expressed in the inner ear

Query Match 4.3%; Score 95.5; DB 2; Length 2120;
Best Local Similarity 24.4%; Pred. No. 46; Mismatches 54; Conservative 28; Indels 72; Gaps 13;
```

```
Qy 115 ASRVLSFDPPFYGHPLRQITATGGFIFMGDVHR-----MLTATQYVAPL---MAN 164
Db 46 SSEIKLSVPRTFPRSPYRTVYVNNNGVISFNSLSVQTPTEAPPLADGRAFAVAPFCGDVAN 105

Qy 165 -----FNP---GYSNSTVVFYDN-----GTVFVQWDHVLQGWEDKSPF-- 202
Db 106 GIRGEIYYRESTNPGLGESSKDIRKFKOMASFSASVWVFTVWEEVQFYG-----GSSTT 161

Qy 203 ---TFQAALHHDG---RIVFAYKEIPMSVPEISSQHPVKTGL-----SDA 242
Db 162 PNTFQAVLITDGVSSFAIFNYQIEISWTGTASGD-PL-TGLGGVMAQAQFNGNINFP 219

Qy 243 FMIL-NPSPDPVESRR-----RSIFEYHRIELDPKSVT 274
Db 220 FSIPGSRTPDIVNIEQTNNVNIPGRWAFKIDGREIDPANLS 260

RESULT 12
I83196
NEDD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: I83196
R;Kumar, S.; Tomooka, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression
A;Reference number: I60167; MUID:92328780; PMID:1378265
A;Accession: I83196
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-708 <RES>
A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetics:
A;Gene: NEDD-4
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin
F;40-77/Domain: WW repeat homology <WW1>
F;196-233/Domain: WW repeat homology <WW2>
F;251-288/Domain: WW repeat homology <WW3>
F;347-682/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 4.3%; Score 95; DB 2; Length 708;
Best Local Similarity 19.3%; Pred. No. 11; Mismatches 91; Conservative 50; Indels 180; Gaps 24;
Matches 91;

Qy 5 QPGAG---HDEGPG---SGWAAKGTVRG---WNRRAESPCHVSPD----- 42
Db 26 QPDAATHLPHPPSPPLPGWEERQDVLGRYYVNHESRRRTQWKRPSPDDDLTDNDMD 85

Qy 43 -----RTQLSDLGSGTGLAMDTLPDNRTR-----VVEDNHSYVSR-LYGPSEP 85
Db 86 QLQAQRAFTTRRQISDVG-----PDNRESPENWEIVRENTESQAVQSPSPG 137

Qy 86 HSRELWVDVAEANRSQVKIHTILSNTHRQASRVLSFDPPFGHPLRQITATGGF 141
Db 138 H-----IDV-----QTH-----LAEFNTRLAVCGNPATSPQVTSNNH 170

Qy 142 IFMGDVIHMLTATQYVAPLMA---ANFNPGY-----SDNSTVVFYDNGTVFVQWDHVL 193
Db 171 SSRGGSLOTCIFEEQPTLPVLLPTSSGLPGWEKQDDRGSRVYVDHNSK-TTWSKPTM 229

Qy 194 Q-----GWEDKSGTFOAALHHDGRIVFAYKEIPMSVPEI 228
Db 230 QDDPRSKI PAHLRGKTDSNDLGPLPQWEER-----THTDGRVFFINHNKKTQWED 281

Qy 229 SSSQHPVKTGLSDAFMILNPSDPVPSR-RSIFEYHRIELDPKSVTSMASAVEFTPLPTC 287
Db 282 PRLQNVATG-----PAPYSRDYKRYKFFFRKLKKQ-----TDIPNK 320

Qy 288 LOHRS CDACMSDILTFNCWCHVLQRCSSGFDYRQSWMDYGCQAQEAECRCEDFQDE-- 345
Db 321 PEMK-----LRRANILEDSTYR-IMGVVRADLLKARLWIEFDGK 360
```

```
Qy 346 -DHDSASP-----TSFSFYDGLTSSSLFIDSLTTEDDTKLNYPAG 388
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 LDYGGVAREWFLLISKEMFNYYG-----LFEYSATDNYTLQINPSG 403
      : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
neprilysin (EC 3.4.24.11) II - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: JC7265
R:Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A:Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and testis
A:Reference number: JC7265
A:Contents: Brain and testis
A:Accession: JC7265
A:Molecule type: mRNA
A:Residues: 1-774 <TAN>
C:Genetics:
A:Gene: nepII
C:Superfamily: neprilysin
C:Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis; tra

Query Match 4.2%; Score 94; DB 2; Length 774;
Best Local Similarity 21.3%; Pred. No. 15;
Matches 82; Conservative 44; Mismatches 123; Indels 136; Gaps 18;

Qy 39 SEPRQTQLSQDLGGTAMDLPNRTVRVEDNHSYVRSYLGSPSPHSRELWVDVAEAN 98
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 SEPLLNVLDL-IGGWPVAMDKW--NET-----MGPKWBLERQLAVLNSQFN 224
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 99 RSQVKIHTLSNTHROASRVLSFDFFPYGHPLRQITATGGTFFMGDVTHRLMTA----- 154
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 R-RVLIDLFIWDDQNSRHYIIDQPTLGMPSRE-----YYFKED-SHRVREAYLQF 275
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 155 -TQYVAPLMAFN-PGYSDNSTVTVYFDNGTVFVQWDHVYLGQWEDKGSFTFQAALHHDG 212
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 MTSVATWLRRLNLPGETD-----LVQ----- 297

Qy 213 RIVPAYKEIPMSVPEISSQHPVKIGLSDAFMILNPSPDVPESRRRSIFE-YHRIELDP- 270
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 298 -----SEMAQVLH-LETHLANA-----TVPQEKRHVDVTLYHRMGLEEL 335
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 271 -----SKVTSNAVEFTPLPTCLOH-----RSCDACMSSDLTFNCS 306
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 QERFGLKGFNWTLPFQNVLSVQVELLPNEEVVYIGIPYLENLEEIIDVFPQATLQNYLV 395

Qy 307 WCHVLQRCSSGFDRYQEWMDYGCA-----QEAEGRMCEDFDQEDHDSA----- 350
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 396 WRLVLDRIGLSLSQRFKEARVDYRKALYGTMTMEEVYRWECVSYVNSNMESAVGSLYIKRAF 455
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 351 SPDTSFSPYDGLTSSSLFIDSL 375
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 SKDS--KSIVSELIEKIRSVFVDNL 478
      : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
S70642
ubiquitin ligase Nedda - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S70642
R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.
EMBO J. 15, 2371-2380, 1996
A:Title: WW domains of Nedda bind to the proline-rich PY motifs in the epithelial Na(+)
A:Reference number: S70642; MUID:96221297; PMID:8665844
A:Accession: S70642
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-887 <STA>
A:Cross-references: UNIPROT:Q62940; EMBL:U50842; NID:g1293646; PIDN:AAB48949.1; PID:g129
C:Genetics:
```

```
A:Gene: Nedda
C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin
F;54-167/Domain: protein kinase C C2 region homology <KC2>
F;246-283/Domain: WW repeat homology <WW1>
F;402-439/Domain: WW repeat homology <WW2>
F;459-496/Domain: WW repeat homology <WW3>
F;555-881/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 4.2%; Score 93.5; DB 2; Length 887;
Best Local Similarity 19.1%; Pred. No. 20;
Matches 90; Conservative 54; Mismatches 151; Indels 175; Gaps 24;

Qy 5 QPGAG-----HDEGPG-----SCWAAKGTVRG-----WNRRARES----- 34
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 QPDAATHLQHPPEPSPPLPGWEERQDVGRTYYVNHESRTQWKPKSPEDDLTDDENGDI 291
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 35 --PGHVSEPRDTQLSQDLGGTAMDLPNRTVR-----VVEDNHSYVRSR-LYGPSEP 85
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 QLQAHGAFTTRRQISEDVDG-----PDNHESPENWEIVREDENTYISGQAVQSPPSG 343
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 86 HSRELWVDVAEANRSQVKIHTLSNTHROASRVLSFDFFPYGHPLRQITATGGTFFMG 145
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 HP-DVQVRLAE-----ELDTRLT-----MYGNPATSQPVTSSNHSRSG 380
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 146 DVIHRLMTATQYVAPLM-----ANFNPGY-----SDNSTVTVYFDNGTVFVQWDHVYLGQ--- 194
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 GSSQTCIFEEQPTLPVLLPTSSGLPGWEEKQDDRGSRYYVDHNSK-TTWSKPTMQDDP 439
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 195 -----GWEDKGSFTFQAALHHDGRIVFAYKAIMPSVPRIS 230
      ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 440 RSKIPAHLRGKTPVDSNDLGLPFGWEER-----THTDGRVFFINHNKKTQWEDPR 491
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 231 SQHPVKTGLSDAFMILNPSPDVPESR-RRSIFEVHRIELDPSSKVTSMASAVEFTPLPTCLO 289
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 492 MQNVAITG-----PAEPYSRDYKRYKRRKLLKQ-----TDIPNKF 530
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 290 HRSDCACMSSDLTFNCSGCHVLRQRCSSGFDRYQEWMDYGCAQEAEGRMCEDFDQED---D 346
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 531 MK-----LRRANILEDYSRR-INGVKRADPLKARLWIEFDGEGKGLD 570
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 347 HDASAPD-----TSFSPYDGLTSSSLFIDSLTTEDDT-KLNYPAG 388
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 571 YGVGVAREWFFLLISKEMFNYYG-----LFEYSATEDNYTLQINPSG 612
      : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
JC2349
protein-tyrosine-phosphatase (SC 3.1.3.48), receptor type N precursor - mouse
N:Alternate names: protein-tyrosine-phosphatase IA-2
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JC2349; S40291; I48721
R:Lu, J.; Notkins, A.L.; Lan, M.S.
Biochem. Biophys. Res. Commun. 204, 930-936, 1994
A:Title: Isolation, sequence and expression of a novel mouse brain cDNA, mTA-2, and its
A:Reference number: JC2349; MUID:95071416; PMID:7980563
A:Accession: JC2349
A:Molecule type: mRNA
A:Residues: 1-979 <LUJ>
A:Cross-references: UNIPROT:Q60673; EMBL:U11812; NID:9563737; PIDN:AAA52102.1; PID:g5637
A:Experimental source: brain
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A:Reference number: S40280
A:Accession: S40291
A:Molecule type: mRNA
A:Residues: 801-837, 839-852, 'T', 854-907 <HEN>
A:Cross-references: EMBL:Z23060; NID:g438157; PIDN:CAA80595.1; PID:g438158
R:Magistralli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
Biochem. Biophys. Res. Commun. 217, 154-161, 1995
A:Title: Expression of PTP35, the murine homologue of the PTP2 se-related sequences 1A-2
A:Reference number: I48721; MUID:96095652; PMID:8526904
```



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:21 ; Search time 139.695 Seconds  
(without alignments)  
1688.701 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_18\_427

Perfect score: 2218

Sequence: 1 ALSFPQAGHDEGPGSGWAA.....GLQNNLSPKTKGTPVHLGTI 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2218	100.0	500	2	Q9HCT9
2	2215	99.9	500	2	Q8IUK5
3	1799.5	81.1	500	2	Q91ZV7
4	1793.5	80.9	500	2	Q9CWV5
5	1780	80.3	507	2	Q8BM20
6	1326	59.8	351	2	Q6ZSC8
7	1326	59.8	351	2	BAC87025
8	1066.5	48.1	529	2	Q6UX71
9	1066.5	48.1	529	2	Q96PD9
10	1066.5	48.1	529	2	AAQ88850
11	1044	47.1	530	2	Q6PFT5
12	1044	47.1	530	2	Q9DC11
13	1044	47.1	530	2	Q91ZV6
14	1044	47.1	530	2	AAH57881
15	1034.5	46.6	513	2	Q6DE92
16	900	40.6	480	2	Q96E59
17	624.5	28.2	625	2	Q9W2V9
18	602	27.1	498	2	Q18500
19	308	13.9	274	2	Q7PFJ6
20	274.5	12.4	384	2	Q7Q2J8
21	253	11.4	77	2	Q7PJF7
22	159.5	7.2	343	2	Q6PVY2
23	159.5	7.2	343	2	AA568255
24	131	5.9	190	2	Q86E23
25	126	5.7	1161	2	Q94901
26	121.5	5.5	2119	2	Q8CJH3
27	117	5.3	308	2	Q9UN94
28	115.5	5.2	1568	2	Q60486
29	114	5.1	1324	2	Q7YZ28
30	111.5	5.0	366	2	Q9UN95
31	111.5	5.0	877	2	Q9H3Q6

ALIGNMENTS

RESULT 1

ID	Q9HCT9	PRELIMINARY;	PRT;	500 AA.
AC	Q9HCT9;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Tumor endothelial marker 7 precursor (tumor endothelial marker 3 precursor)			
DE	Name=TEM7;			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
OX	[1]			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=20407466; PubMed=10947988;			
RA	St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E., Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B., Kinzler K.W.;			
RA	"Genes expressed in human tumor endothelium.";			
RL	Science 289:1197-1202(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	St Croix B., Vogelstein B., Kinzler K.W.;			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21443268; PubMed=11559528;			
RA	Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B., Kinzler K.W., St Croix B.;			
RA	"Cell surface tumor endothelial markers are conserved in mice and humans.";			
RL	Cancer Res. 61:6649-6655(2001).			
DR	EMBL; AF279144; AAC00869.2; -			
DR	EMBL; AF378753; AAL11990.1; -			
DR	GO; GO:0001525; P:angiogenesis; NAS.			
DR	InterPro; IPR003659; Plexin-like.			
DR	InterPro; IPR002165; Plexin_repeat.			
DR	Pfam; PF01437; PSI; 1.			
DR	SMART; SMO0423; PSI; 1.			
DR	Signal.			
KW	SIGNAL			
FT	CHAIN 19 500			
FT	SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;			
SQ	SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;			

Query Match 100.0%; Score 2218; DB 2; Length 500;

Best Local Similarity 100.0%; Pred. No. 4.2e-174;

Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALSFPQAGHDEGPGSGWAAKGTVRNRRARESPGHVSEPDRTQLSQDLGGGTLMDTL 60

Db 18 ALSFPQAGHDEGPGSGWAAKGTVRNRRARESPGHVSEPDRTQLSQDLGGGTLMDTL 77

Qy 61 PDNRTRVEDNHSYVYSLYGPSPHSHRELWVDVAENRSQVKIHTILSNTHRQASRVL 120  
 Db 78 PDNRTRVEDNHSYVYSLYGPSPHSHRELWVDVAENRSQVKIHTILSNTHRQASRVL 137  
 Qy 121 SFDFPFYGHPLRQITITATGGIFMGDVHHRMLTATQVAPLMAFNFGYSDNSTVVYFDN 180  
 Db 138 SFDFPFYGHPLRQITITATGGIFMGDVHHRMLTATQVAPLMAFNFGYSDNSTVVYFDN 197  
 Qy 181 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
 Db 198 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
 Qy 241 DAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVFTPLPTCLQHRSCDACWSSD 300  
 Db 258 DAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVFTPLPTCLQHRSCDACWSSD 317  
 Qy 301 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRCMEDFQDEHDSASPDTSFSPYD 360  
 Db 318 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRCMEDFQDEHDSASPDTSFSPYD 377  
 Qy 361 GDLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410  
 Db 378 GDLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 427

## RESULT 2

Q81UKS ID Q81UKS PRELIMINARY; PRT; 500 AA.  
 AC Q81UKS;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Plexin domain containing 1,  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis" of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC036059; AAH36059.1; --  
 DR Genew; HGNC:20945; PLXDC1.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin\_repeat.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00423; PSI; 1.  
 SQ SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;  
 Query Match 99.9%; Score 2215; DB 2; Length 500;  
 Best Local Similarity 99.8%; Pred. No. 7.5e-174;  
 Matches 409; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ALSFPQAGHDEGPGSGAAAKGTVRGWNRRAARESPGHVSEPDRTQLSQDLGGGTLMADTLL 60  
 Db 18 ALSFPQAGHDEGPGSGAAAKGTVRGWNRRAARESPGHVSEPDRTQLSQDLGGGTLMADTLL 77  
 Qy 61 PDNRTRVEDNHSYVYSLYGPSPHSHRELWVDVAENRSQVKIHTILSNTHRQASRVL 120  
 Db 78 PDNRTRVEDNHSYVYSLYGPSPHSHRELWVDVAENRSQVKIHTILSNTHRQASRVL 137  
 Qy 121 SFDFPFYGHPLRQITITATGGIFMGDVHHRMLTATQVAPLMAFNFGYSDNSTVVYFDN 180  
 Db 138 SFDFPFYGHPLRQITITATGGIFMGDVHHRMLTATQVAPLMAFNFGYSDNSTVVYFDN 197  
 Qy 181 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 240  
 Db 198 GTVFVQWDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257  
 Qy 241 DAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVFTPLPTCLQHRSCDACWSSD 300  
 Db 258 DAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVFTPLPTCLQHRSCDACWSSD 317  
 Qy 301 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRCMEDFQDEHDSASPDTSFSPYD 360  
 Db 318 LTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRCMEDFQDEHDSASPDTSFSPYD 377  
 Qy 361 GDLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 410  
 Db 378 GDLTTSSSLFIDSLTETDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTI 427  
 RESULT 3  
 Q91ZV7 ID Q91ZV7 PRELIMINARY; PRT; 500 AA.  
 AC Q91ZV7;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Tumor endothelial marker 7 precursor.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21443268; PubMed=11559528;  
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,  
 RA Kinzler K.W., St Croix B.;  
 RT "Cell surface tumor endothelial markers are conserved in mice and  
 RT humans";  
 RL Cancer Res. 61:6649-6655 (2001).  
 DR EMBL; AF378760; AAL11997.1; --  
 DR MGD; MGI:1919574; Plxdc1.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003659; plexin-like.  
 DR InterPro; IPR002165; plexin\_repeat.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00423; PSI; 1.  
 RW Signal.  
 KW SIGNAL.  
 FT CHAIN  
 SQ SEQUENCE 500 AA; 55693 MW; 14FE25512A319DAF CRC64;



```

Query Match      81.1%; Score 1799.5; DB 2; Length 500;
Best Local Similarity 80.7%; Pred. No. 1.3e-139;
Matches 331; Conservative 39; Mismatches 39; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGSRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78

Qy 61 PDNTRVVEDNHSYVYVSRVYGPSEPHSRELWVDVAEANRSQVKITHILSNTHRSQSRVVL 120
Db 79 PDNTRVVEDNHNHYVSRVYGPSEPHSRELWVDVAEANRSQVKITHILSNTHRSQSRVVL 138

Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRLMTATQVAPLMAFNFGYSDNSTVYVFDN 180
Db 139 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRLMTATQVAPLMAFNFGYSDNSTVYVFDN 198

Qy 181 GTVFVQWQDHVYLVQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKLS 240
Db 199 GTVFVQWQDHVYLVQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKLS 258

Qy 241 DAFMILNPSDPVPSRRRSRRIPEYHRIELDPSSKVTSMGSAVEFTPLPTCQLHRSQCDACMSDD 300
Db 259 DAFMILNPSDPVPSRRRSRRIPEYHRIELDPSSKVTSMGSAVEFTPLPTCQLHRSQCDACMSDD 318

Qy 301 LTFNCSWCHVLCRCSSGFDRIYRQWMDYVGCQAEGRMCEDFQDEHDSASPTDSFSPYD 360
Db 379 GD-STTSSSLFIDSLTETDDTKLNPYAGDGLPDHSSPKSGKPPVHLGTI 427

RESULT 4
Q9CWV5 PRELIMINARY; PRT; 500 AA.
AC Q9CWV5;
AT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
DE clone:2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
GN Name=Plxdc1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.";
RT Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RA prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RA sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK010361; BAB26881.1; -.
DR MGD; MGI:1919574; Plxdc1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like
DR InterPro; IPR003659; Flexin-like.
DR InterPro; IPR002165; Plexin-repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;

Query Match      80.9%; Score 1793.5; DB 2; Length 500;
Best Local Similarity 80.5%; Pred. No. 4.2e-139;
Matches 330; Conservative 39; Mismatches 40; Indels 1; Gaps 1;

Qy 1 ALSPOGAGHDEGPGSCWAAKGTVRGNRRARESPGHVSEPDRTQLSQDLGGGTAMDTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGSRRRPRESPAQVLKPGKTQLSQDLGGGSLAIDTL 78

Qy 61 PDNTRVVEDNHSYVYVSRVYGPSEPHSRELWVDVAEANRSQVKITHILSNTHRSQSRVVL 120
Db 79 PDNTRVVEDNHNHYVSRVYGPSEPHSRELWVDVAEANRSQVKITHILSNTHRSQSRVVL 138

Qy 121 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRLMTATQVAPLMAFNFGYSDNSTVYVFDN 180
Db 139 SFDPFFYGHPLRQITTIATGGFIFMGDVIHRLMTATQVAPLMAFNFGYSDNSTVYVFDN 198

Qy 181 GTVFVQWQDHVYLVQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKLS 240
Db 199 GTVFVQWQDHVYLVQWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKLS 258

Qy 241 DAFMILNPSDPVPSRRRSRRIPEYHRIELDPSSKVTSMGSAVEFTPLPTCQLHRSQCDACMSDD 300
Db 259 DAFMILNPSDPVPSRRRSRRIPEYHRIELDPSSKVTSMGSAVEFTPLPTCQLHRSQCDACMSDD 318

Qy 301 LTFNCSWCHVLCRCSSGFDRIYRQWMDYVGCQAEGRMCEDFQDEHDSASPTDSFSPYD 360
Db 379 GD-STTSSSLFIDSLTETDDTKLNPYAGDGLPDHSSPKSGKPPVHLGTI 427

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319 LTFNCWCHVLCRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPDSSFPFN 378
361 GDLTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGTPVHLGTI 410
379 GD-STTSSSLFIDSLTTEDDTKLNYPYAGDGLPDHSSPKSGKPPVHLGTI 427

RESULT 5
Q8BM20
ID Q8BM20 PRELIMINARY; PRT; 507 AA.
AC Q8BM20;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER 7
DE homolog.
GN Name=Plxcl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN R1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN R2
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
[3]
RN R3
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Hayashizaki Y.;
RA Konno H., Okazaki Y., Muramatsu M., Sugahara Y., Shibata K., Itoh M.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN R4
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11078861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsuono H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN R5
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

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RA Hori F., Imotani K., Ieshii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK036144; BAC29318.1; -.
DR MGD; MGI:1919574; Plxcl1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; InterPro07110; Ig-like.
DR InterPro; InterPro03659; Plexin-like.
DR InterPro; InterPro02165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;
Query Match 80.3%; Score 1780; DB 2; Length 507;
Best Local Similarity 79.1%; Pred. No. 5.5e-138;
Matches 330; Conservative 39; Mismatches 40; Indels 8; Gaps 2;
Qy 1 ALSPOGAGHDEGPGCGAAKGTVRGWRREARSPGHVSFDRDTLSQDLGGGTLMADTL 60
Db 19 ALSPATPAGHNEGQDSAWTAKTRQGSRRPRSPQVLPKPKTKQLSQDLGGGSLADTL 78
Qy 61 PDNRTRVV-----EDNHYVYSLYGPSEPHSRRLWVDVAENRSQVKIHTLSNTHR 113
Db 79 PDNRTRVVALSLSPQEDNHNHYVYRVVYGPCKQSQDLAVDLAVANRSHVKIHLSSSHR 138
Qy 114 QASRVLSFDPFPYGHPLRQITATGFIPIGMDVIHMLTATQVAPLPMANFPGYSDNS 173
Db 139 QASRVLSFDPFPYGHPLRQITATGFIPIGMDVHMLTATQVAPLPMANFPGYSDNS 198
Qy 174 TVYFDNGTVVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQH 233
Db 199 TVAYFDNGTVVQWDHVLQDREDGSGFTFOALHHDGRIVFAYKEIPMAVLDISSAQH 258
Qy 234 PVKTGLSDAFMLNPSDPVPESSRRSIFEYHRIELDPKVTSMASAVEFTPLTCLQHRSC 293
Db 259 PVKAGLSDAFMLNPSDEVPASQRTTFEYHRELDSSKITTSAVEFTPLTCLQHQSC 318
Qy 294 DACMSSDLTFNCWCHVLCRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDHDSASPD 353
Db 319 DTCVSSNLTFNCWCHVLCRCSSGFDYRQEWLTYGCAQAEAGKTCEDFQDDSHYSASPD 378
Qy 354 TSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGTPVHLGTI 410
Db 379 SSFSPFNGD-STTSSSLFIDSLTTEDDTKLNYPYAGDGLPDHSSPKSGKPPVHLGTI 434

RESULT 6
Q6ZSC8
ID Q6ZSC8 PRELIMINARY; PRT; 351 AA.
AC Q6ZSC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45632.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN R1
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Youki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ieshii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,

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Qy 234 PVKTLGSDAFVWVHRLNPSDPVPSRRRSIFEXHRIELDPKSVMSAVFTPLPTCLQHRSC 293
Db 275 PVKGLGSDAFVWVHRIQIIPNRRRTIYEHVRVQLQMSKIINISAVEMTPLPTCLQFNRC 334
Qy 294 DACMSSDLTFCNSCHVLQRCSSGFDYRQEMWMDYGCABEAGRMCMDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGFDHRQDWDVSGCPESKCKMCMTEPVTSSRTTT 394
Qy 354 T--SFSPYDGLTFTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTVPVHL 407
Db 395 TVGATTTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDDSAEKKGGTLHA 454
Qy 408 GTI 410
Db 455 GLI 457

RESULT 9
Q96PD9 PRELIMINARY; PRT; 529 AA.
ID Q96PD9 PRELIMINARY; PRT; 529 AA.
AC Q96PD9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN Name="TEM7R";
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655 (2001).
DR EMBL; AF378757; AAL11994.1; -.
DR Genew; HGNC:21013; PLXDC2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;

Query Match 48.1%; Score 1066.5; DB 2; Length 529;
Best Local Similarity 56.5%; Pred. No. 3.8e-79;
Matches 205; Conservative 63; Mismatches 88; Indels 7; Gaps 4;

Qy 55 LAMDTLPDNRTRVVED-NHSYVSRLYGSPSEPHSRELWVDVAENRSQVKIHTLSNTHR 113
Db 95 LLLDDGQDNNTQIEEDTDHNYISRIYGPSDSASRDLWVNIQWQEKVKVHGLSNTHR 154
Qy 114 QASRVVLSFDPFPFGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMANFNPGYSDNS 173
Db 155 QAARVNLSFDPFPFGHFLREITVATGGFIYGEVHRLMTATQYIAPLMANFDPVSRNS 214
Qy 174 TVVYFDNGTVFVQWQDHVYLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 233
Db 215 TVRYFDNGTALVQWQDHVHLQDNYNLGSGFTFQATLLMDGRIIFGYKEIPVLVTQISSTNH 274
Qy 234 PVKTLGSDAFVWVHRLNPSDPVPSRRRSIFEXHRIELDPKSVMSAVFTPLPTCLQHRSC 293
Db 275 PVKGLGSDAFVWVHRIQIIPNRRRTIYEHVRVQLQMSKIINISAVEMTPLPTCLQFNRC 334
Qy 294 DACMSSDLTFCNSCHVLQRCSSGFDYRQEMWMDYGCABEAGRMCMDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGFDHRQDWDVSGCPESKCKMCMTEPVTSSRTTT 394
Qy 354 T--SFSPYDGLTFTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTVPVHL 407
Db 395 TVGATTTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDDSAEKKGGTLHA 454

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Qy 294 DACMSSDLTFCNSCHVLQRCSSGFDYRQEMWMDYGCABEAGRMCMDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGFDHRQDWDVSGCPESKCKMCMTEPVTSSRTTT 394
Qy 354 T--SFSPYDGLTFTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTVPVHL 407
Db 395 TVGATTTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDDSAEKKGGTLHA 454
Qy 408 GTI 410
Db 455 GLI 457

RESULT 10
AAQ88850 PRELIMINARY; PRT; 529 AA.
ID AAQ88850 PRELIMINARY; PRT; 529 AA.
AC AAQ88850;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ARFP2514.
GN UNQ2514.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270 (2003).
DR EMBL; AY358486; AAQ88850.1; -.
SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;

Query Match 48.1%; Score 1066.5; DB 2; Length 529;
Best Local Similarity 56.5%; Pred. No. 3.8e-79;
Matches 205; Conservative 63; Mismatches 88; Indels 7; Gaps 4;

Qy 55 LAMDTLPDNRTRVVED-NHSYVSRLYGSPSEPHSRELWVDVAENRSQVKIHTLSNTHR 113
Db 95 LLLDDGQDNNTQIEEDTDHNYISRIYGPSDSASRDLWVNIQWQEKVKVHGLSNTHR 154
Qy 114 QASRVVLSFDPFPFGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMANFNPGYSDNS 173
Db 155 QAARVNLSFDPFPFGHFLREITVATGGFIYGEVHRLMTATQYIAPLMANFDPVSRNS 214
Qy 174 TVVYFDNGTVFVQWQDHVYLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 233
Db 215 TVRYFDNGTALVQWQDHVHLQDNYNLGSGFTFQATLLMDGRIIFGYKEIPVLVTQISSTNH 274
Qy 234 PVKTLGSDAFVWVHRLNPSDPVPSRRRSIFEXHRIELDPKSVMSAVFTPLPTCLQHRSC 293
Db 275 PVKGLGSDAFVWVHRIQIIPNRRRTIYEHVRVQLQMSKIINISAVEMTPLPTCLQFNRC 334
Qy 294 DACMSSDLTFCNSCHVLQRCSSGFDYRQEMWMDYGCABEAGRMCMDFQDEHDSASPD 353
Db 335 GPCVSSQIGFNCSCWCKLQRCSSGFDHRQDWDVSGCPESKCKMCMTEPVTSSRTTT 394
Qy 354 T--SFSPYDGLTFTTS---SSLFIDSLLTDDTKLNPYAGDGLQ--NNLSPKTKGTVPVHL 407
Db 395 TVGATTTQFRVLTTTTRRAVTSQPTSLPTEDDTKIALHLKDNKGASTDDSAEKKGGTLHA 454

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QY 408 GTI 410
DB 455 GLI 457

RESULT 11
Q6PETS PRELIMINARY; PRT; 530 AA.
AC Q6PETS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Tumor endothelial marker 7-related.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis"
RT and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Straube R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057881; AAH57881.1;
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;

Query Match 47.1%; Score 1044; DB 2; Length 530;
Best Local Similarity 51.3%; Pred. No. 2.7e-77;
Matches 203; Conservative 67; Mismatches 112; Indels 14; Gaps 6;

QY 27 WNRARSPGHVSPDRQLSQ----DLGGTGLAMDTLPDRTRVED-NHSYVSLRYG 81
DB 65 WKRNV--DPFKAVDTNRASMGQASPEKSGFTDLLDDGQNNNTQIEDTDHNYISRYG 122

QY 82 PSEPHSRLVDVAEANRSQVKIHTILSNTHRQASRVVLSDFPFYGHPLRQITATGCF 141
DB 123 PADASRDVLWNIDQMEKDKVKIHLGILSNTHRQARVNLSDFPFYGHFLNEVITATGCF 182

QY 142 IFMGDVIHRLMTATQYVAPLMAFNPNPGVSDNSTVVFYDNGTVFVQMDHVLQGWDEKGS 201
DB 183 IYTGVEVHRLMTATQYIAPLMAFNPNPGVSDNSTVVFYDNGTVFVQMDHVLQDNYNLGS 242

QY 202 FTFOALHHDCRIYFAYKEIPMSVPEITSSSHOPKVTGLSDAFMLINSPDPVPSRRSIF 261
DB 243 FTFOALLMDGRIIFGYKEIPVLVTQISSTNHPKVLGSLDAFVNVHRIQIPNVRRRTY 302
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262 EYHRIELDPKSVTSMASVEFTPLPTCLQHRSCDAMGSDLTFCNSWCHVLCRCSSGPDY 321
DB 303 EYHVELQMSKITNISAVEMTPLPTCLQFNGCGPCVSSQIGFNCWSCKLQRCSSGPDH 362

QY 322 ROEMWDYCCAQAEAG--RMCEDFQDEHDHDSASPTSPYDGLTTS----SSLFIDSL 375
DB 363 RQDWVDGCPPEVQSKMKCKTBPGETSQTTTSHTTTMOFRVLTTTTRRAVTSQMTSL 422

QY 376 TTEDDTKLNPYAGGDLQ--NNLSPKTKGTPVHLGTI 410
DB 423 PTEDDTKIALHKDSGASTDSDSAEKKGGTLHAGLI 458

RESULT 12
Q9DC11 PRELIMINARY; PRT; 530 AA.
AC Q9DC11;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
DE homolog.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
```



RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057881; AAH57881; -;  
SQ SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;  
  
Query Match 47.1%; Score 1044; DB 2; Length 530;  
Best Local Similarity 51.3%; Pred. No. 2.7e-77;  
Matches 203; Conservative 67; Mismatches 112; Indels 14; Gaps 6;  
  
QY 27 WNRARSPGHVSEPDRTQLSQ-----DLGGTGLAMDITLPDNRTRVED-NHSYVVSRLYLG 81  
DB 65 WKRNVDVVAEANRSQVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGF 122  
  
QY 82 PSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGF 141  
DB 123 PADSASRDLWNIDOMEKVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGF 182  
  
QY 142 IFMGDVLHRLMTATQYVAPLMAFNPGVSDNSTVYFDNGTALVQVQDHLQNYNLGS 201  
DB 183 IYGEVVRHMLTATQYVAPLMAFNPGVSDNSTVYFDNGTALVQVQDHLQNYNLGS 242  
  
QY 202 FTFOALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIF 261  
DB 243 FTFOATLMDGRIFVAYKEIPVLTQISSTNHPVKVGLSDAFVVRHRIQIPNVRRTIV 302  
  
QY 262 EYHRIELDPKVTSMASVEFTPLTCLQHRSCDMSDLTFNCSWCHVLRCSGGFDY 321  
DB 303 EYHRIELDPKVTSMASVEFTPLTCLQHRSCDMSDLTFNCSWCHVLRCSGGFDY 362  
  
QY 322 ROEMMDYGCQAEG--RMCEDFODEHDSASPDTSFSPYDGLTTS---SSLFTDSL 375  
DB 363 RQMDVSDGCEPEVOSKEMKEKTEPGTSTQTTTSHHTTQVFRVLTTRRAVTSQMPSTL 422  
  
QY 376 TTEDDTKLNPYAGDGLQ--NNLSPKTKGTPVHLGTI 410  
DB 423 PTEDDTKLALHDKSGASTDSDAAEKKGGTILHAGLI 458  
  
RESULT 15  
Q6DE92 ID Q6DE92 PRELIMINARY; PRT; 513 AA.  
AC Q6DE92;  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxId=8355;

RNA SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Klein S., Strausberg R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC077242; AAH77242.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 513 AA; 57622 MW; 301EA53F2905A4ED CRC64;  
  
Query Match 46.6%; Score 1034.5; DB 2; Length 513;  
Best Local Similarity 51.3%; Pred. No. 1.6e-76;  
Matches 200; Conservative 69; Mismatches 106; Indels 15; Gaps 5;  
  
QY 27 WNRARSPGHVSEPDRTQLSQDLGGTGLAMDITLPDNRTRVED-NHSYVVSRLYGPSEP 85  
DB 61 WKRSQVDV-----NRPSVQDF--PDMFEGTNGEIEEDTHKYTSRYTGYPLDS 111  
  
QY 86 HSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGFIMG 145  
DB 112 ASRDLWNIDOMEKVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITATGGFIMG 171  
  
QY 146 DVTHRLMTATQYVAPLMAFNPGVSDNSTVYFDNGTALVQVQDHLQNYNLGSSTFFQ 205  
DB 172 EVHRLMTATQYVAPLMAFNPGVSDNSTVYFDNGTALVQVQDHLQNYNLGSSTFFQ 231  
  
QY 206 AALHHDGRIVFAYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHR 265  
DB 232 ATLINDGRIVFGYKIDIPVPMQISSTNHPVKVGLSDAFVVRHRIQIPNVRRTIFEYHR 291  
  
QY 266 IELDPKVTSMASVEFTPLTCLQHRSCDMSDLTFNCSWCHVLRCSGGFDYRQEW 325  
DB 292 VELEMTKITSFSAVEMPLATCLQFNCSWCHVLRCSGGFDYRQEW 351  
  
QY 326 MDYGCQAEGRCEDPDQ-----EDHDSASPDTSFSPYDGLTTSSTSLFIDSITTEDDT 381  
DB 352 VENGTEESKDTVCDDLQTTGISHHTTGLHATTSTIYAFITTTTMRMASHFSPNLTEDDT 411  
  
QY 382 KLNPYAGDGLQ--NNLSPKTKGTPVHLGTI 410  
DB 412 KIALHLKNDGASTDSDAAEKKGGTILHAGLI 441

Search completed: January 28, 2005, 22:11:23  
Job time : 141.695 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:21 ; Search time 22.1468 Seconds  
(without alignments)  
1688.701 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344

Perfect score: 370

Sequence: 1 YHRIELDPKVTSMASVEFT.....CHVLQRCSGFDRIYRQEWMD 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	500	2	Q8IUK5
2	370	100.0	500	2	Q9HCT9
3	325	87.8	500	2	Q9CWT5
4	325	87.8	500	2	Q91ZV7
5	325	87.8	507	2	Q8BM20
6	287	77.6	351	2	Q8ZSC8
7	287	77.6	351	2	BAC87025
8	264	71.4	530	2	Q6PET5
9	264	71.4	530	2	Q9DC11
10	264	71.4	530	2	Q91ZV6
11	264	71.4	530	2	AAH57881
12	263	71.1	480	2	Q96E59
13	263	71.1	529	2	Q6UX71
14	263	71.1	529	2	Q96PD9
15	263	71.1	529	2	AAQ88850
16	251	67.8	513	2	Q6DE92
17	172	46.5	625	2	Q9W2V9
18	137	37.0	498	2	Q18500
19	101	27.3	1568	2	Q60486
20	100.5	27.2	384	2	Q7Q2J8
21	90.5	24.5	2119	2	Q8CJH3
22	84	22.7	1764	2	O45657
23	84	22.7	1764	2	CAB05755
24	83.5	22.6	729	2	Q9UJ93
25	83.5	22.6	835	2	Q6DCP0
26	83.5	22.6	1832	2	Q6XN20
27	83.5	22.6	1832	2	AAH66773
28	83.5	22.6	1952	2	Q9UJ92
29	83.5	22.6	2135	2	Q9UIV7
30	83.5	22.6	2143	2	O43157
31	82.5	22.3	506	2	P90641

Q8C3X9 mus musculus  
Q8CGW1 mus musculus  
Q9QZC2 mus musculus  
Q86E23 schistosoma  
Q6PYV2 schistosoma  
AA68255 schistosoma  
PS1805 homo sapien  
Q9UIW1 homo sapien  
Q76915 bos taurus  
BAD05055 bos taurus  
O75051 homo sapien  
P70208 mus musculus  
Q91823 xenopus lae  
Q6YBW0 trichinella

## ALIGNMENTS

RESULT 1  
Q8IUK5 PRELIMINARY; PRT; 500 AA.  
AC Q8IUK5;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Plexin domain containing 1,  
GN Name=PLXDC1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC036059; AAH36059.1; -;  
DR Genew; HGNC:20945; PLXDC1.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR InterPro; IPR003659; Plexin-like.  
DR Pfam; PF01437; PSI; 1.  
DR SMART; SM00423; PSI; 1.  
SQ SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;

Query Match 100.0%; Score 370; DB 2; Length 500;





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RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK036144; BAC29318.1; -.
DR MGD; MGI:191574; Plx1dcl.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;

Query Match 87.8%; Score 325; DB 2; Length 507;
Best Local Similarity 84.4%; Pred. No. 6.9e-30;
Matches 54; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 60
Db 288 YHVELDSSKTTTTSVAVEFTPLPTCLOHRSQCDTVCSSNLTFCNSCHVLCRCSSGFD 347

Qy 61 QEWM 64
Db 348 QEWL 351

RESULT 6
ID Q6ZSC8 PRELIMINARY; PRT; 351 AA.
AC Q6ZSC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45632.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 77.6%; Score 287; DB 2; Length 351;
Best Local Similarity 91.2%; Pred. No. 1.5e-25;
Matches 52; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 57
Db 273 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 329

RESULT 7
ID Q6ZSC8 PRELIMINARY; PRT; 351 AA.
AC Q6ZSC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45632.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 77.6%; Score 287; DB 2; Length 351;
Best Local Similarity 91.2%; Pred. No. 1.5e-25;
Matches 52; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 57
Db 273 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 329

RESULT 7
ID BAC87025 PRELIMINARY; PRT; 351 AA.
AC BAC87025;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ45632 fig. clone CHON2001834, highly similar to Homo sapiens
DE tumor endothelial marker 7 (TEM7).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mueashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 77.6%; Score 287; DB 2; Length 351;
Best Local Similarity 91.2%; Pred. No. 1.5e-25;
Matches 52; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 57
Db 273 YHRIELDPKVTSMASAVEFTPLPTCLOHRSQCDACMSSDLTFCNSCHVLCRCSSGFD 329

RESULT 8
ID Q6PETS PRELIMINARY; PRT; 530 AA.
AC Q6PETS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor endothelial marker 7-related.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Basak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057881; AAHS7881.1; -.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.

```



[illegible]

05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE ARFP2514.  
 GN ORFNames=UNQ2514;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358486; AAQ88850.1; -.  
 DR InterPro; IPR003659; Plexin-like.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00423; PSI; 1.  
 SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;  
 Query Match 71.1%; Score 263; DB 2; Length 529;  
 Best Local Similarity 67.7%; Pred. No. 1.5e-22;  
 Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 YHRIELDPKVTMSAVEFTPLTCLQHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60  
 Db 304 YHRVELQMSKITNISAVEMTFLPTCLQPNRCPCVSSQIGFNCSCWCKLQRCSSGFDHR 363  
 Qy 61 QEWMND 65  
 Db 364 QDWVD 368  
 RESULT 14  
 ID Q96PD9 PRELIMINARY; PRT; 529 AA.  
 AC Q96PD9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Tumor endothelial marker 7-related precursor.  
 GN Name=TM78;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21443268; PubMed=11559528;  
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,  
 RA Kinzler K.W., St Croix B.;  
 RT "Cell surface tumor endothelial markers are conserved in mice and  
 RT humans.";  
 RL Cancer Res. 61:6649-6655(2001).  
 DR EMBL; AF378757; AAL11994.1; -.  
 DR Genew; HGNC:21013; FLXDC2.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007275; P:development; IEA.  
 DR InterPro; IPR003659; Plexin-like.  
 DR InterPro; IPR002165; Plexin\_repeat.  
 DR Pfam; PF01437; PSI; 1.  
 DR SMART; SM00423; PSI; 1.

KW Signal.  
 FT SIGNAL 1 30 Potential.  
 FT CHAIN 31 529 tumor endothelial marker 7-related.  
 SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;  
 Query Match 71.1%; Score 263; DB 2; Length 529;  
 Best Local Similarity 67.7%; Pred. No. 1.5e-22;  
 Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 YHRIELDPKVTMSAVEFTPLTCLQHRSCDACMSSDLTFCNSCHVLCRCSSGFDYR 60  
 Db 304 YHRVELQMSKITNISAVEMTFLPTCLQPNRCPCVSSQIGFNCSCWCKLQRCSSGFDHR 363  
 Qy 61 QEWMND 65  
 Db 364 QDWVD 368  
 RESULT 15  
 ID AAQ88850 PRELIMINARY; PRT; 529 AA.  
 AC AAQ88850;  
 DT 02-MAR-2004 (TREMBlrel. 27, Created)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
 DE ARFP2514.  
 GN UNQ2514.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A  
 RT Bioinformatics Assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358486; AAQ88850.1; -.  
 SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;  
 Query Match 71.1%; Score 263; DB 2; Length 529;  
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 Db 304 YHRVELQMSKITNISAVEMTFLPTCLQPNRCPCVSSQIGFNCSCWCKLQRCSSGFDHR 363  
 Qy 61 QEWMND 65  
 Db 364 QDWVD 368  
 Search completed: January 28, 2005, 22:11:21  
 Job time : 23.1468 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:55:58 ; Search time 4.50139 Seconds  
(without alignments)  
1389.370 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_280\_344  
Perfect score: 370  
Sequence: 1 YHRIELDPKVTSMASVEFT.....CHVLQRCSGFDYRQEWMD 65  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	37.0	476	2 T19786	hypothetical prote
2	101	27.3	1568	2 T09074	semaphorin recepto
3	84	22.7	1806	2 T23298	hypothetical prote
4	77.5	20.9	1872	2 JC4976	plexin 3 precursor
5	76.5	20.7	1905	2 T51553	Plexin - African c
6	76	20.5	1884	2 JC4975	plexin 2 precursor
7	75	20.3	1945	2 T13937	plexin A - fruit f
8	74	20.0	1894	2 JC4980	plexin 1 precursor
9	70	18.9	1379	1 S01254	hepatocyte growth
10	69.5	18.8	465	2 D88448	protein C45G9.8 [i
11	69	18.6	444	2 G84565	probable flavonol
12	68	18.4	1390	1 TVHUME	hepatocyte growth
13	67.5	18.2	1375	2 T30813	plasminogen relate
14	67.5	18.2	2051	2 T13164	plexin B - fruit f
15	67	18.1	174	2 G81349	periplasmic nitrat
16	67	18.1	1375	1 JC5148	hepatocyte growth
17	65	17.6	1425	2 T30811	hepatocyte growth
18	64.5	17.4	413	2 H75070	sugar-phosphate nu
19	64.5	17.4	1291	2 T21694	hypothetical prote
20	64	17.3	470	2 H84565	probable flavonol
21	63.5	17.2	846	2 A30889	integrin beta chai
22	63	17.0	1404	1 A48196	protein-tyrosine k
23	62.5	16.9	439	2 S33293	testican - human
24	62.5	16.9	491	2 S31784	VP5 protein - bovi
25	62.5	16.9	712	2 T27165	hypothetical prote
26	62.5	16.9	774	2 G71308	probable aminopept
27	62.5	16.9	1042	2 T16169	hypothetical prote
28	61	16.5	210	2 S76973	hypothetical prote
29	61	16.5	3938	2 T42761	Bassoon protein -

30 Bassoon protein -  
31 hypothetical prote  
32 hypothetical conse  
33 hypothetical prote  
34 hypothetical prote  
35 probable membrane  
36 protein-tyrosine k  
37 protein F3M18.14 {  
38 probable SET-domai  
39 hypothetical prote  
40 hypothetical prote  
41 salivary protein 1  
42 probable zinc fing  
43 hypothetical prote  
44 probable sugar-pho  
45 probable C2H2-type

ALIGNMENTS

RESULT 1

T19786  
hypothetical protein C36E8.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T19786  
R;Wilkinson, J.; Barlow, K.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: Z19177  
A;Accession: T19786  
A;Status: preliminary; translated from GE/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-476 <WIL>  
A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3  
C;Genetics:  
A;Map position: 3  
A;Gene: CESP:C36E8.3  
A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2  
C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 37.0%; Score 137; DB 2; Length 476;  
Best Local Similarity 37.0%; Pred. No. 8.4e-08;  
Matches 27; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 1 YHRIELDPKVTSMASVEFTPLPTCLOHRSQDACMSSDLT-FNCSCWCHVLQR-----CS- 53  
Db 297 YHRIETAAQKIVSNTVILKAQPTCTISFDTCTNATLPHFNCMLWCHAKKSHGGPFCTD 356

Qy 54 -SGFDYRQEWMD 65

Db 357 EAGLHRRRQHWFE 369

RESULT 2

T09074

semaphorin receptor VESPR - human

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: T09074

R;Comeau, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Geating, P.; van den Bos, T.; P

Immunity 8, 473-482, 1998

A;Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and bi

A;Reference number: Z16555; MUID:98246049; PMID:9586637

A;Accession: T09074

A;Status: preliminary; translated from GE/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-1568 <COM>

A;Cross-references: UNIPROT:O60486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3

A;Experimental source: tissue type foreskin; cell type fibroblast

C;Genetics:

A;Gene: VESPR



C;Genetics:  
A;Gene: plexA  
A;Cross-references: FlyBase:FBgn0025741  
A;Map position: 4  
C;Function:  
A;Description: may function as repellents during axon guidance  
C;Keywords: cell adhesion; nerve

Query Match 20.3%; Score 75; DB 2; Length 1945;  
Best Local Similarity 44.8%; Pred. No. 2.7;  
Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

Qy 25 CLQHRSCDACMSSDLTFNCSWCHVLQRC 53  
Db 672 CSTHSSCTRCVSSB--FPDCMVCBAHRC 698

RESULT 8  
JC4980  
plexin 1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 09-Jul-2004  
C;Accession: JC4980  
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 524-529, 1996  
A;Title: Identification of a neuronal cell surface molecule, plexin, in mice.  
A;Reference number: JC4980; MUID:96400291; PMID:8806667  
A;Accession: JC4980  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1894 <KAM>  
A;Cross-references: UNIPROT:P70206; DDBJ:D86948; NID:gl65756; PIDN:BAA13188.1; PID:d101  
A;Experimental source: brain  
C;Comment: This protein is a membrane protein, and plays a role in neuronal cell contact  
ence of calcium ions.  
C;Keywords: duplication; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;513-561,659-704,807-859/Region: cysteine-rich  
F;1238-1264/Domain: transmembrane #status predicted <TMM>  
F;1266-1268/Region: hydrophilic

Query Match 20.0%; Score 74; DB 2; Length 1894;  
Best Local Similarity 44.0%; Pred. No. 3.4;  
Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 29 RSCDACMSSDLTFNCSWCHVLQRC 53  
Db 812 QSCGLCLKADPRFCGVCVAERCS 836

RESULT 9  
S01254  
hepatocyte growth factor receptor precursor - mouse  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) met  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S01254; JH0115; A45453  
R;Chan, A.M.L.; King, H.W.S.; Deakin, E.A.; Tempest, P.R.; Hilkens, J.; Kroezen, V.; Edw  
Oncogene 2, 593-599, 1988  
A;Title: Characterization of the mouse met proto-oncogene.  
A;Reference number: S01254; MUID:88262253; PMID:2838789  
A;Accession: S01254  
A;Molecule type: mRNA  
A;Residues: 1-1379 <CHA>  
A;Cross-references: UNIPROT:P16056; EMBL:Y00671; NID:G53058; PIDN:CAA68680.1; PID:G53059  
R;Wilks, A.F.; Kurban, R.R.; Hovens, C.M.; Ralph, S.J.  
Gene 85, 67-74, 1989  
A;Title: The application of the polymerase chain reaction to cloning members of the prot  
A;Reference number: JH0112; MUID:90152381; PMID:2482828  
A;Accession: JH0115  
A;Molecule type: mRNA  
A;Residues: 1',1200-1254, 'R',1256-1260, 'T',1262-1268 <WIL>  
A;Experimental source: hemopoietic cell

A;Note: the authors translated the codon ACG for residue 1261 as Lys  
R;Weidner, K.M.; Sachs, M.; Birchmeier, W.  
J. Cell Biol. 121, 145-154, 1993  
A;Title: The Met receptor tyrosine kinase transduces motility, proliferation, and morpho  
A;Reference number: A45453; MUID:93209981; PMID:8384622  
A;Accession: A45453  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
C;Genetics:  
A;Gene: met  
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology  
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-925/Domain: extracellular #status predicted <EXT>  
F;25-302/Product: hepatocyte growth factor receptor alpha chain #status predicted <ACH>  
F;308-1379/Product: hepatocyte growth factor receptor beta chain #status predicted <BCH>  
F;930-954/Domain: transmembrane #status predicted <TMM>  
F;955-1379/Domain: intracellular #status predicted <INT>  
F;1074-1342/Domain: protein kinase homology <KIN>  
F;1082-1090/Region: protein kinase ATP-binding motif  
F;1108/Active site: Lys #status predicted  
F;1233/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict

Query Match 18.9%; Score 70; DB 1; Length 1379;  
Best Local Similarity 30.4%; Pred. No. 7.2;  
Matches 14; Conservative 5; Mismatches 19; Indels 8; Gaps 2;

Qy 18 EFTPLPT----CLQHRSCDACMSSDLTFNCSWCH----VLQRCSSG 55  
Db 508 KITKIPLNGLCGHFGQSCQLSAPYFIQCQWCHNCVRFDPCPSG 553

RESULT 10  
D88448  
protein C45G9.8 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: D88448  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A;Reference number: A75000; MUID:99089613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: D88448  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-465 <STO>  
A;Cross-references: UNIPROT:Q09280; GB:chr\_III; PIDN:AAA62551.1; PID:g687873; GSPDB:GN00  
C;Genetics:  
A;Gene: C45G9.8  
A;Map position: 3

Query Match 18.8%; Score 69.5; DB 2; Length 465;  
Best Local Similarity 30.0%; Pred. No. 3.1;  
Matches 18; Conservative 10; Mismatches 31; Indels 1; Gaps 1;

Qy 3 RIELFSKVTSMGAVETPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDYRQE 62  
Db 56 RMQIDRLRRSTEHVEIVPOETCVHHESPDVLTFCATMSTS-THVMPNSSLSTSKGATE 114

RESULT 11  
G84565  
probable flavonol 3-O-glucosyltransferase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G84565  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vautken, S.E.; Unayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: G84565  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-444 <NTO>  
A;Cross-references: UNIPROT:Q92U71; GB:A8002093; NID:G4218003; PIDN:AAD12211.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g18560  
A;Map position: 2  
C;Superfamily: flavonol O3-glucosyltransferase

Query Match 18.6%; Score 69; DB 2; Length 444;  
Best Local Similarity 24.6%; Pred. No. 3.4; Mismatches 26; Indels 10; Gaps 2;  
Matches 16; Conservative 13

Qy 6 LDPKSVKTSMAVEPTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSG-----FDRYR 60  
Db 303 LDRTRGVGLVVTQWAPQVEILSHRSIGGFLS-----HCGWSSVLESITKGVPIIAWPLYA 357  
Qy 61 QEWMD 65  
Db 358 EQWMN 362

RESULT 12  
TVRUME  
hepatocyte growth factor receptor precursor - human  
N;Contains: protein-tyrosine kinase (SC 2.7.1.112) met  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1991 #sequence revision 30-Sep-1992 #text change 09-Jul-2004  
C;Accession: A40175; A28303; A93749; A93369; A53761; 157632; A30008; B24569  
R;Giordano, S.  
submitted to the EMBL Data Library, November 1990  
A;Reference number: A40175  
A;Accession: A40175  
A;Molecule type: mRNA  
A;Residues: 1-1390 <GIO>  
A;Cross-references: UNIPROT:P08581; EMBL:X54559  
R;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6379-6383, 1987  
A;Title: Sequence of MET protooncogene cDNA has features characteristic of the tyrosine  
A;Reference number: A28303; MUID:87317655; PMID:2819873  
A;Accession: A28303  
A;Molecule type: mRNA  
A;Residues: 1-755; 'TWKBPNTIVSLFPCAS', 756-1190, 'A', 1192-1390 <PAR>  
A;Cross-references: GB:J02958; NID:G187558; PIDN:AAA59591.1; PID:G307196  
R;Chan, A.M.L.; King, H.W.S.; Tempest, P.R.; Deakin, E.A.; Cooper, C.S.; Brookes, P.  
Oncogene 1, 229-233, 1987  
A;Title: Primary structure of the met protein tyrosine kinase domain.  
A;Reference number: A93749; MUID:88143699; PMID:3325883  
A;Accession: A93749  
A;Molecule type: mRNA  
A;Residues: 'VNEYRECQSLRLKLNQKALTEKKNLEIAQDRNIAIQSQ', 'FTRTKEELEAKRDLIRTNRLSQELEY  
A;Cross-references: GB:U08818; NID:G487741; PIDN:AA860323.1; PID:G487742  
A;Note: this activated met oncogene is the product of gene rearrangement  
R;Dean, M.; Park, M.; Le Beau, M.M.; Robins, T.S.; Diaz, M.O.; Rowley, J.D.; Blair, D.G.  
Nature 318, 385-388, 1985  
A;Title: The human met oncogene is related to the tyrosine kinase oncogenes.  
A;Reference number: A93369; MUID:86065462; PMID:4069211  
A;Accession: A93369  
A;Molecule type: DNA  
A;Residues: 1267-1390 <DEA>  
A;Cross-references: GB:M35074; NID:G187555; PIDN:AAA59590.1; PID:G386868  
R;Gambartorta, G.; Piatoli, S.; Giordano, S.; Comoglio, P.M.; Santoro, C.  
J. Biol. Chem. 269, 12852-12857, 1994  
A;Title: Structure and inducible regulation of the human MET promoter.  
A;Reference number: A53761; MUID:94230365; PMID:8175700  
A;Accession: A53761  
A;Molecule type: mRNA  
A;Residues: 1-14 <GAM>  
R;Ferracini, R.; Longati, P.; Naldini, L.; Vigna, E.; Comoglio, P.M.  
J. Biol. Chem. 266, 19558-19564, 1991

A;Title: Identification of the major autophosphorylation site of the Met/hepatocyte growth  
A;Reference number: A40179; MUID:92011756; PMID:1655790  
A;Contents: annotation; autophosphorylation site  
R;Dean, M.; Park, M.; Vande Woude, G.F.  
Mol. Cell. Biol. 7, 921-924, 1987  
A;Title: Characterization of the rearranged tpr-met oncogene breakpoint.  
A;Reference number: 157632; MUID:87144265; PMID:3821733  
A;Accession: 157632  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 963-1009 <RES>  
A;Cross-references: GB:M15325; NID:G187531; PIDN:AAA59585.1; PID:G187532  
C;Comment: The receptor is a dimer of disulfide-bonded 50K alpha and 145K beta chains th  
C;Genetics:  
A;Gene: GDB:MET  
A;Cross-references: GDB:120178; OMIM:164860  
A;Map position: 7q31-7q31  
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology  
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-303/Product: hepatocyte growth factor receptor alpha chain #status predicted <ALP>  
F;308-1390/Product: hepatocyte growth factor receptor beta chain #status predicted <BET>  
F;933-955/Domain: transmembrane #status predicted <TMN>  
F;1076-1344/Domain: protein kinase homology <KIN>  
F;1084-1092/Region: protein kinase ATP-binding motif  
F;45,106,149,202,399,405,635,785,930/Binding site: carbohydrate (Asn) (covalent) #status  
F;1110/Active site: Lys #status experimental  
F;1235/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experim

Query Match 18.4%; Score 68; DB 1; Length 1390;  
Best Local Similarity 30.4%; Pred. No. 12; Mismatches 18; Indels 8; Gaps 2;  
Matches 14; Conservative 6

Qy 18 EFTPLPT-----CLQHRSCDACMSSDLTFNCSCWCH-----VLQRCSSG 55  
Db 509 KITKIPLNGLGCRHFRQSCQLSAPPFVQCGWCHDKVCRSECLSG 554

RESULT 13  
T30813  
plasmaingen related growth factor receptor 2 - Fugu rubripes  
C;Species: Fugu rubripes  
C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: T30813  
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, M.; Elgar, G.  
FEBS Lett. 443, 370-374, 1999  
A;Title: Three receptor genes for plasmaingen related growth factors in the genome of th  
A;Reference number: Z20880; MUID:99148833; PMID:10025966  
A;Accession: T30813  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1375 <COT>  
A;Cross-references: UNIPROT:Q9YGM5; EMBL:AJ010348; NID:ei1355080; PID:ei1355082; PIDN:CAAO  
C;Genetics:  
A;Gene: PRGR2  
A;Introns: 400/3; 459/3; 499/3; 556/3; 611/2; 655/3; 701/2; 761/2; 794/3; 870/3; 919/3;  
C;Superfamily: hepatocyte growth factor receptor; protein kinase homology

Query Match 18.2%; Score 67.5; DB 2; Length 1375;  
Best Local Similarity 32.4%; Pred. No. 14; Mismatches 14; Indels 7; Gaps 1;  
Matches 12; Conservative 4

Qy 10 KVTSMGAVEPTPLPTCLQHRSCDACMSSDLTFNCSCW 46  
Db 502 KVPVSLG-----PGCAHFRTCSCLMAPRFMNCGWC 531

RESULT 14  
T13164  
plexin B - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C:Accession: T13164  
R:Winberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie  
Cell 95, 903-916, 1998  
A:Title: Plexin A is a neuronal semaphorin receptor that controls axon guidance.  
A:Reference number: Z17621; MUID:99091049; PMID:9875845  
A:Accession: T13164

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2051 <MIN>  
A:Cross-references: UNIPROT:O96682; EMBL:AF106933; NID:g4056675; PID:g4056676; PIDN:AA00

C:Genetics:  
A:Gene: plexB

A:Cross-references: FlyBase:FBgn0025740  
A:Map position: 4

C:Function:  
A:Description: plays a role in neuronal cell contact, axon guidance and fasciculation

Query Match 18.2%; Score 67.5; DB 2; Length 2051;  
Best Local Similarity 28.8%; Pred. No.19;  
Matches 15; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

Qy 6 LDPSK---VTMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLRCS 53

Db 513 MSPKDFLYVLRSQKIKLRIEHCSTVNTCSACLESRDPP-CGWCSLEKRCT 563

## RESULT 15

G81349

Periplasmic nitrate reductase small chain (cytochrome C-type protein) Cj0783 [imported]  
C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: G81349

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: G81349

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <PAR>

A:Cross-references: UNIPROT:Q9PPD6; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7304

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: napB; Cj0783

C:Superfamily: cytochrome c-type protein napB

Query Match 18.1%; Score 67; DB 2; Length 174;  
Best Local Similarity 42.9%; Pred. No. 2.5;  
Matches 15; Conservative 2; Mismatches 14; Indels 4; Gaps 1;

Qy 20 TPLPTC---LQHRSCDACMSSDLTFNCSCWCHVLQ 50

Db 105 TPLPASHYDFRNKTTGDMISDRFNCTQCHVPQ 139

Search completed: January 28, 2005, 22:12:42  
Job time : 7.50139 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2005, 21:59:20 ; Search time 29.518 Seconds  
(without alignments)  
1321.880 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_137\_244

Perfect score: 588

Sequence: 1 LSFDFPYGHPLRQITATG.....LHNDGRIVFAYKEIPMSVPE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588	100.0	240	14	US-10-104-047-3712
2	588	100.0	431	10	US-09-912-935-36
3	588	100.0	431	14	US-10-168-365-36
4	588	100.0	488	17	US-10-357-819-4
5	588	100.0	500	10	US-09-918-715-230
6	588	100.0	500	15	US-10-435-696-79
7	588	100.0	500	17	US-10-474-794-230
8	588	100.0	500	17	US-10-357-819-2
9	588	100.0	502	14	US-10-156-487A-5
10	588	100.0	1002	10	US-09-918-715-179
11	588	100.0	1002	17	US-10-474-794-179
12	528	89.8	500	10	US-09-918-715-192
13	528	89.8	500	10	US-09-918-715-297

14	528	89.8	500	14	US-10-156-487A-6	Sequence 6, Appli
15	528	89.8	500	17	US-10-474-794-192	Sequence 192, App
16	528	89.8	500	17	US-10-474-794-297	Sequence 297, App
17	417	70.9	392	10	US-09-912-935-23	Sequence 23, Appl
18	417	70.9	392	10	US-09-912-935-25	Sequence 25, Appl
19	417	70.9	392	14	US-10-168-365-23	Sequence 25, Appl
20	417	70.9	392	14	US-10-168-365-25	Sequence 25, Appl
21	417	70.9	425	10	US-09-912-935-35	Sequence 35, Appl
22	417	70.9	425	14	US-10-168-365-35	Sequence 35, Appl
23	417	70.9	449	10	US-09-912-935-34	Sequence 34, Appl
24	417	70.9	449	14	US-10-168-365-34	Sequence 34, Appl
25	417	70.9	499	10	US-09-912-935-31	Sequence 31, Appl
26	417	70.9	499	14	US-10-168-365-31	Sequence 31, Appl
27	417	70.9	529	10	US-09-918-715-189	Sequence 189, App
28	417	70.9	529	10	US-09-918-715-200	Sequence 200, App
29	417	70.9	529	10	US-09-912-935-28	Sequence 28, Appl
30	417	70.9	529	10	US-09-912-935-40	Sequence 40, Appl
31	417	70.9	529	13	US-10-052-586-472	Sequence 472, App
32	417	70.9	529	13	US-10-066-500-128	Sequence 128, App
33	417	70.9	529	14	US-10-174-590-472	Sequence 472, App
34	417	70.9	529	14	US-10-176-758-472	Sequence 472, App
35	417	70.9	529	14	US-10-175-737-472	Sequence 472, App
36	417	70.9	529	14	US-10-174-581-472	Sequence 472, App
37	417	70.9	529	14	US-10-176-483-472	Sequence 472, App
38	417	70.9	529	14	US-10-176-749-472	Sequence 472, App
39	417	70.9	529	14	US-10-176-914-472	Sequence 472, App
40	417	70.9	529	14	US-10-176-915-472	Sequence 472, App
41	417	70.9	529	14	US-10-173-706-472	Sequence 472, App
42	417	70.9	529	14	US-10-175-738-472	Sequence 472, App
43	417	70.9	529	14	US-10-175-752-472	Sequence 472, App
44	417	70.9	529	14	US-10-176-482-472	Sequence 472, App
45	417	70.9	529	14	US-10-176-757-472	Sequence 472, App

#### ALIGNMENTS

##### RESULT 1

US-10-104-047-3712  
; Sequence 3712, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 3712  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3712

Query Match 100.0%; Score 588; DB 14; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.4e-60;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LSFDFPYGHPLRQITATGTFPMGDVIRHMLTATQYVAPLMAFNPGYSDNSTVVYFD 60  
Db 64 LSFDFPYGHPLRQITATGTFPMGDVIRHMLTATQYVAPLMAFNPGYSDNSTVVYFD 123  
Qy 61 NGTVFVQWDRHYLQGHEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108  
Db 124 NGTVFVQWDRHYLQGHEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 171

##### RESULT 2

US-09-912-935-36  
; Sequence 36, Application US/09912935

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; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-912-935-36

Query Match      100.0%; Score 588; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 66 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 125

Qy 61 NGTVFVQWHDVHYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 126 NGTVFVQWHDVHYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 173

RESULT 3
US-10-168-365-36
; Sequence 36, Application US/10168365
; Publication No. US20030211987A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Childs, John
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Mize, Nancy
; APPLICANT: Lee, Jui
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 30266/37630
; CURRENT APPLICATION NUMBER: US/10/168.365
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-365-36

Query Match      100.0%; Score 588; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.9e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 66 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 125

Qy 61 NGTVFVQWHDVHYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 126 NGTVFVQWHDVHYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 173

RESULT 4
US-10-357-819-4
; Sequence 4, Application US/10357819
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; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Raestelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-539A
; CURRENT APPLICATION NUMBER: US/10/357.819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,367
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: Curasequist version 0.1
; SEQ ID NO 4
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-357-819-4

Query Match      100.0%; Score 588; DB 17; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.4e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 137 LSPDFPFYGHPLRQITATGTFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 196

Qy 61 NGTVFVQWHDVHYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWHDVHYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 5
US-09-918-715-230
; Sequence 230, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
```



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; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-230

Query Match      100.0%; Score 588; DB 10; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 137 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 196

Qy 61 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 6
US-10-435-696-79
; Sequence 79, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; FILE REFERENCE: LeA 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-79

Query Match      100.0%; Score 588; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 137 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 196

Qy 61 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 7
US-10-474-794-230
; Sequence 230, Application US/10474794
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; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-230

Query Match      100.0%; Score 588; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 137 LSPDFPPYGHPLRQITTIATGCFIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 196

Qy 61 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 8
US-10-357-819-2
; Sequence 2, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Svytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
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Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 192
LENGTH: 500
TYPE: PRT
ORGANISM: Mus musculus
US-09-918-715-192

Query Match      89.8%; Score 528; DB 10; Length 500;
Best Local Similarity 91.5%; Pred. No. 3.9e-53;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 60
Db 138 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 197

Qy 61 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
Db 198 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMAV 243

RESULT 13
US-09-918-715-297
Sequence 297, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918.715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 297
LENGTH: 500
TYPE: PRT
ORGANISM: Mouse
US-09-918-715-297

Query Match      89.8%; Score 528; DB 10; Length 500;
Best Local Similarity 91.5%; Pred. No. 3.9e-53;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 60
Db 138 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 197

Qy 61 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
Db 198 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMAV 243
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RESULT 14
US-10-156-487A-6
Sequence 6, Application US/10156487A
Publication No. US20030092025A1
GENERAL INFORMATION:
APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Oliner, John
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156.487A
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/293,852
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 500
TYPE: PRT
ORGANISM: Mus musculus
US-10-156-487A-6

Query Match      89.8%; Score 528; DB 14; Length 500;
Best Local Similarity 91.5%; Pred. No. 3.9e-53;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 60
Db 138 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 197

Qy 61 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
Db 198 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMAV 243

RESULT 15
US-10-474-794-192
Sequence 192, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474.794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 192
LENGTH: 500
TYPE: PRT
ORGANISM: Mus musculus
US-10-474-794-192

Query Match      89.8%; Score 528; DB 17; Length 500;
Best Local Similarity 91.5%; Pred. No. 3.9e-53;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 60
Db 138 LSPDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQVAPLMAFNPNFGYSDNSTVYFD 197

Qy 61 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
Db 198 NGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMAV 243
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Job time : 33.518 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run-on: January 28, 2005, 21:56:43 ; Search time 8.77562 Seconds  
(without alignments)  
816.164 Million cell updates/sec

Title: US-09-918-715-230\_COPY\_137\_244

Perfect score: 588

Sequence: 1 LSFDFPYGHLRQITATG.....LHHDGRIVFAYKEIPMSVPE 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	100.0	431	4	US-09-912-935-36
2	417	70.9	392	4	US-09-764-325A-23
3	417	70.9	392	4	US-09-764-325A-25
4	417	70.9	392	4	US-09-912-935-23
5	417	70.9	392	4	US-09-912-935-25
6	417	70.9	425	4	US-09-912-935-35
7	417	70.9	449	4	US-09-912-935-34
8	417	70.9	499	4	US-09-912-935-31
9	417	70.9	529	4	US-09-912-935-28
10	417	70.9	529	4	US-09-912-935-40
11	411	69.9	530	4	US-09-912-935-38
12	68	11.6	324	1	US-08-746-797-2
13	68	11.6	324	1	US-08-927-387-2
14	68	11.6	324	2	US-08-918-058-2
15	67	11.4	254	4	US-09-543-681A-7887
16	67	11.4	613	4	US-09-252-991A-19955
17	66	11.2	410	4	US-09-540-236-3584
18	66	11.2	454	4	US-09-450-209-16
19	66	11.2	738	3	US-08-989-385-1
20	66	11.2	738	4	US-09-593-826-1
21	65.5	11.1	262	4	US-09-543-681A-4675
22	64	10.9	363	3	US-09-195-666A-4
23	64	10.9	363	3	US-09-635-705-4
24	64	10.9	363	4	US-09-634-858A-4
25	64	10.9	363	4	US-08-869-927C-4
26	64	10.9	424	6	5169835-6
27	64	10.9	450	4	US-09-270-767-46295

28	64	10.9	565	3	US-09-008-481A-6	Sequence 6, Appli
29	64	10.9	565	3	US-09-195-666A-5	Sequence 5, Appli
30	64	10.9	565	3	US-09-195-666A-49	Sequence 49, Appli
31	64	10.9	565	3	US-09-309-592-6	Sequence 6, Appli
32	64	10.9	565	3	US-09-635-705-5	Sequence 5, Appli
33	64	10.9	565	3	US-09-635-705-49	Sequence 49, Appli
34	64	10.9	565	4	US-09-634-858A-5	Sequence 5, Appli
35	64	10.9	565	4	US-09-634-858A-49	Sequence 49, Appli
36	64	10.9	565	4	US-08-869-927C-5	Sequence 5, Appli
37	64	10.9	565	4	US-08-869-927C-49	Sequence 49, Appli
38	64	10.9	609	4	US-09-257-525A-9	Sequence 9, Appli
39	63.5	10.8	78	3	US-09-011-540-6	Sequence 6, Appli
40	63.5	10.8	377	2	US-08-929-922B-2	Sequence 2, Appli
41	63.5	10.8	377	3	US-09-342-394-2	Sequence 2, Appli
42	63.5	10.8	377	3	US-09-580-064-2	Sequence 2, Appli
43	63.5	10.8	377	3	US-09-011-540-2	Sequence 2, Appli
44	63.5	10.8	377	4	US-09-718-709-2	Sequence 2, Appli
45	63	10.7	220	4	US-09-583-110-2877	Sequence 2877, Ap

## ALIGNMENTS

RESULT 1  
US-09-912-935-36  
; Sequence 36, Application US/09912935  
; Patent No. 6673904  
; GENERAL INFORMATION:  
; APPLICANT: Nishikawa, Mitsuo et al.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: 32066/37483  
; CURRENT APPLICATION NUMBER: US/09/912.935  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: PCT/US00/35260  
; PRIOR FILING DATE: 2000-12-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-935-36

Query Match		100.0%;	Score 588;	DB 4;	Length 431;
Best Local Similarity		100.0%;	Pred. No. 2e-66;		
Matches 108;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	LSFDFPYGHLRQITATG	IFMGDVHRLMTATQVAPL	MANFPGYSDNSTVYFD	60
Db	66	LSFDFPYGHLRQITATG	IFMGDVHRLMTATQVAPL	MANFPGYSDNSTVYFD	125
Qy	61	NGTVFVQWDRHYLQGWEDKGSFT	QALHHDGRIVFAYKEIPMSVPE	108	
Db	126	NGTVFVQWDRHYLQGWEDKGSFT	QALHHDGRIVFAYKEIPMSVPE	173	

RESULT 2  
US-09-764-325A-23  
; Sequence 23, Application US/09764325A  
; Patent No. 6667391  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Tang, Y. T.  
; APPLICANT: Chao, Cheng-Chi  
; APPLICANT: Mize, Nancy K.  
; APPLICANT: Childs, John  
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell  
; FILE REFERENCE: 30266/37630A  
; CURRENT APPLICATION NUMBER: US/09/764.325A  
; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 09/547,358
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 09/545,714
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-325A-23

Query Match 70.9%; Score 417; DB 4; Length 392;
Best Local Similarity 72.2%; Pred. No. 1.1e-44;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSFDPFPGHPLROITATGCFPMGDVHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 24 LSFDPFPGHFLREITVATGCFYTGVEVHRMLTATQYIAPLMAFNDFPSVSRNSTVRYFD 83

Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Db 84 NGTALVQWDHVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQ 131

RESULT 3
US-09-764-325A-25
; Sequence 25, Application US/09764325A
; Patent No. 6667391
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Tang, Y. T.
; APPLICANT: Chao, Cheng-Chi
; APPLICANT: Mize, Nancy K.
; APPLICANT: Childs, John
; TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
; FILE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
; FILE REFERENCE: 30266/37630A
; CURRENT APPLICATION NUMBER: US/09/764,325A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/547,358
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 09/545,714
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-325A-25

Query Match 70.9%; Score 417; DB 4; Length 392;
Best Local Similarity 72.2%; Pred. No. 1.1e-44;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSFDPFPGHPLROITATGCFPMGDVHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 24 LSFDPFPGHFLREITVATGCFYTGVEVHRMLTATQYIAPLMAFNDFPSVSRNSTVRYFD 83

Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Db 84 NGTALVQWDHVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQ 131

RESULT 4
US-09-912-935-23
; Sequence 23, Application US/09912935

; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-23

Query Match 70.9%; Score 417; DB 4; Length 392;
Best Local Similarity 72.2%; Pred. No. 1.1e-44;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSFDPFPGHPLROITATGCFPMGDVHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 24 LSFDPFPGHFLREITVATGCFYTGVEVHRMLTATQYIAPLMAFNDFPSVSRNSTVRYFD 83

Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Db 84 NGTALVQWDHVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQ 131

RESULT 5
US-09-912-935-25
; Sequence 25, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-25

Query Match 70.9%; Score 417; DB 4; Length 392;
Best Local Similarity 72.2%; Pred. No. 1.1e-44;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSFDPFPGHPLROITATGCFPMGDVHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
Db 24 LSFDPFPGHFLREITVATGCFYTGVEVHRMLTATQYIAPLMAFNDFPSVSRNSTVRYFD 83

Qy 61 NGTVFVQWDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPE 108
Db 84 NGTALVQWDHVHLQDNYNLGSGFTFOATLLMDGRIIFGYKEIPVLVTQ 131

RESULT 6
US-09-912-935-35
; Sequence 35, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

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, APPLICANT: Nishikawa, Mitsuo et al.
, TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
, TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
, FILE REFERENCE: 32066/37483
, CURRENT APPLICATION NUMBER: US/09/912,935
, CURRENT FILING DATE: 2001-07-24
, PRIOR APPLICATION NUMBER: PCT/US00/35260
, PRIOR FILING DATE: 2000-12-23
, NUMBER OF SEQ ID NOS: 53
, SOFTWARE: PatentIn version 3.0
, SEQ ID NO 40
, LENGTH: 529
, TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-912-935-40

Query Match      70.9%; Score 417; DB 4; Length 529;
Best Local Similarity 72.2%; Pred. No. 1.6e-44;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSFDPFFYGHPLRQITTIATGGFIFMGDVHRLMTATQYVAPLMANFNFGYSDNSTVVYFD 60
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Db 161 LSFDPFFYGHFLREITVATGGFIYTGVEVVHRLMTATQYIAPLMANFDSVSRNSTVRYFD 220

Qy 61 NGTVFVVQWDHVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 NGTALVVQWDHVHLQDNYNLGSFTFQAATLLMDGRIIFGYKEIPVLVTQ 268

RESULT 11
US-09-912-935-38
; Sequence 38, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
US-09-912-935-38

Query Match      69.9%; Score 411; DB 4; Length 530;
Best Local Similarity 70.4%; Pred. No. 9.5e-44;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 LSFDPFFYGHPLRQITTIATGGFIFMGDVHRLMTATQYVAPLMANFNFGYSDNSTVVYFD 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 161 LSFDPFFYGHFLNEVTATGGFIYTGVEVVHRLMTATQYIAPLMANFDSVSRNSTVRYFD 220

Qy 61 NGTVFVVQWDHVYLGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 NGTALVVQWDHVHLQDNYNLGSFTFQAATLLMDGRIIFGYKEIPVLVTQ 268

RESULT 12
US-08-746-797-2
; Sequence 2, Application US/08746797
; Patent No. 5759832
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel
; APPLICANT: Lonsdale, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: NOVEL FabH
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,797
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5759832 Yet Assigned
; FILING DATE: 23-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50573
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-746-797-2

Query Match      11.6%; Score 68; DB 1; Length 324;
Best Local Similarity 23.5%; Pred. No. 2.6;
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;

Qy 15 ITIATGGFIFMGDVHRLMTATQYVAPLMANFNPG-----YSDNSTVVYFDN 61
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 108 LTAACSGFVF-----ALSTA EKPIA--SGRFQKGLVIGSETLSKAVDWSDRSTAVLFGD 159

Qy 62 GTVPVW-----QWDHVYLGWEDKGS-----FTFQAA-----LHHDGRIV-- 96
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 160 GAGGVLLAESEQEHFLAESLNSDGRSECLTYGHSLGHSPLSDQESADSLFKMDGRIVFD 219

Qy 97 FAYKEIPMSVPE 108
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 220 FAIRDVAKSINQ 231

RESULT 13
US-08-927-387-2
; Sequence 2, Application US/08927387
; Patent No. 5783432
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel
; APPLICANT: Lonsdale, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: NOVEL FabH
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,387
; FILING DATE: 25-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/746,797  
FILING DATE: 23-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmi, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50573  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 324 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-927-387-2

Query Match 11.6%; Score 68; DB 1; Length 324;  
Best Local Similarity 23.5%; Pred. No. 2.6;  
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;  
Qy 15 ITIATGGFIEMGDVHRMLTATQYVAPLMAFNFG-----YSDNSTVWYFDN 61  
Db 108 LTAACSGFV-----ALSTAETKFA--SGRFQGLVIGSETLSKAVDWSRSTAVLFGD 159  
Qy 62 GTVFV-----QWDHVYLQGWEDKGS-----FTFQAA-----LHHDGRIV-- 96  
Db 160 GAGGVILLEASQEHFLAESLNSDGRSCLTYGHSLGHSFPDQESADSFLKMDGRTVFD 219  
Qy 97 PAYKEIPMSVPE 108  
Db 220 FAIRDVAKSINQ 231

RESULT 14  
US-08-918-058-2  
Sequence 2, Application US/08918058  
Patent No. 5885572  
GENERAL INFORMATION:  
APPLICANT: Gentry, Daniel  
APPLICANT: Lonsdale, John  
APPLICANT: Payne, David  
APPLICANT: Pearson, Stewart  
TITLE OF INVENTION: NOVEL FABH  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/918,058  
FILING DATE: 25-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/746,797  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmi, Edward R  
REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P50573  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 324 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-918-058-2

Query Match 11.6%; Score 68; DB 2; Length 324;  
Best Local Similarity 23.5%; Pred. No. 2.6;  
Matches 31; Conservative 19; Mismatches 36; Indels 46; Gaps 7;  
Qy 15 ITIATGGFIEMGDVHRMLTATQYVAPLMAFNFG-----YSDNSTVWYFDN 61  
Db 108 LTAACSGFV-----ALSTAETKFA--SGRFQGLVIGSETLSKAVDWSRSTAVLFGD 159  
Qy 62 GTVFV-----QWDHVYLQGWEDKGS-----FTFQAA-----LHHDGRIV-- 96  
Db 160 GAGGVILLEASQEHFLAESLNSDGRSCLTYGHSLGHSFPDQESADSFLKMDGRTVFD 219  
Qy 97 PAYKEIPMSVPE 108  
Db 220 FAIRDVAKSINQ 231

RESULT 15  
US-09-543-681A-7887  
Sequence 7887, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 7887  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-7887

Query Match 11.4%; Score 67; DB 4; Length 254;  
Best Local Similarity 26.5%; Pred. No. 2.5;  
Matches 22; Conservative 15; Mismatches 30; Indels 16; Gaps 3;  
Qy 16 TIATGGFIEMGDVHRMLTATQYVAPL--MANFNPGYSDNSTVWYFDNGTVFVQ----- 68  
Db 135 SIKTGGILIGEPYWRQIPTTQETIAQACGASSISDFLTLSLAVVSFDNQGYDLVEMVLAD 194  
Qy 69 ---WDH-----VYLGWEDKGS 82  
Db 195 QEGWDRYEAAKMTMRRLDKNS 217

Search completed: January 28, 2005, 22:14:13  
Job time : 10.0256 secs

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Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	588	100.0	351	2	Q6ZSC8	Q6zac8 homo sapien
2	588	100.0	351	2	BAC97025	Bac87025 homo sapi
3	588	100.0	500	2	Q9HCT9	Q9hct9 homo sapien
4	585	99.5	500	2	Q8IUK5	Q8iuk5 homo sapien
5	528	89.8	500	2	Q9CWW5	Q9cww5 mus musculu
6	528	89.8	500	2	Q91ZV7	Q91zv7 mus musculu
7	528	89.8	507	2	Q8BM20	Q8bm20 mus musculu
8	417	70.9	480	2	Q9GE59	Q9ge59 homo sapien
9	417	70.9	529	2	Q6UX71	Q6ux71 homo sapien
10	417	70.9	529	2	Q9GPD9	Q9gpd9 homo sapien
11	417	70.9	529	2	AAQ88850	AAQ88850 homo sapi
12	413	70.2	513	2	Q6DE92	Q6de92 xenopus lae
13	411	69.9	530	2	Q6PBT5	Q6pet5 mus musculu
14	411	69.9	530	2	Q9DC11	Q9dc11 mus musculu
15	411	69.9	530	2	Q91ZV6	Q91zv6 mus musculu
16	411	69.9	530	2	AAH57881	AAH57881 mus muscu
17	317.5	54.0	498	2	Q1B500	Q1b500 caenorhabdi
18	304	51.7	625	2	Q9W2V9	Q9w2v9 drosophila
19	249	42.3	77	2	Q7RFJ7	Q7rfj7 anopheles g
20	220.5	37.5	274	2	Q7RJF6	Q7rjf6 anopheles g
21	210.5	35.8	384	2	Q7Q2J8	Q7q2j8 anopheles g
22	123	20.9	1161	2	Q04901	Q04901 halocynthia
23	87.5	14.9	1324	2	Q7FY28	Q7fy28 cryptospori
24	86	14.6	1538	2	Q7FPF6	Q7fpf6 anopheles g
25	86	14.6	2323	2	Q7Q1V0	Q7q1v0 anopheles g
26	84.5	14.4	315	2	Q6URR8	Q6urr8 xenopus lae
27	84.5	14.4	315	2	AAQ62573	AAQ62573 xenopus l
28	84	14.3	121	1	SHH_CARAU	P79691 carassius a
29	84	14.3	121	1	SHH_PUNCO	P79838 puntius con
30	84	14.3	121	1	SHH_PUNTE	P79850 puntius tet
31	84	14.3	121	1	SHH_RASEL	P79858 rasbora ele

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RN
RP
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mubashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuoka K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Maeuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 100.0%; Score 588; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 6.8e-54;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
Db 130 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 189

Qy 61 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 190 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 237

RESULT 3
Q9HCT9
ID Q9HCT9 PRELIMINARY; PRT; 500 AA.
AC Q9HCT9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE precursor endothelial marker 7 precursor (Tumor endothelial marker 3
DE precursor).
GN Name=TEM7;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RA Kinzler K.W.;
RA Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RA "Genes expressed in human tumor endothelium.";
RL Science 289:1197-1202(2000).
[2]
RN
RP
RA St Croix B., Vogelstein B., Kinzler K.W.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN
RP
RA Kinzler K.W.;
RA Kinzler K.W., St Croix B.;
RA "Cell surface tumor endothelial markers are conserved in mice and
RA humans.";
RL Cancer Res. 61:6649-6655(2001).
RL EMBL; AF279144; AAG00869.2; -.
DR EMBL; AF378753; AAL11990.1; -.
DR GO; GO:0001525; P:angiogenesis; NAS.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 500 tumor endothelial marker 3.
SQ SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;
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RN
RP
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Mubashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
RA Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
RA Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuoka K.,
RA Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Maeuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127539; BAC87025.1; -.
SQ SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;

Query Match 100.0%; Score 588; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
Db 137 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 196

Qy 61 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
Db 197 NGTVFVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244

RESULT 4
Q8IUUK5
ID Q8IUUK5 PRELIMINARY; PRT; 500 AA.
AC Q8IUUK5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Plexin domain containing 1,.
GN Name=PLXDC1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN
RP
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gramwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP
RA Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036059; AAH36059.1; -.
DR Genew; HGNC:20945; PLXDC1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;

Query Match 99.5%; Score 585; DB 2; Length 500;
Best Local Similarity 99.1%; Pred. No. 2.1e-53;
Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGGFIFMGDVHHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
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Db 137 LSPDFPPYGHPLRQITATGCGTIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 196
Qy 61 NGTVFVVQWDHVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
    |||||
Db 197 NGTVFVVQWDHVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244
    |||||

RESULT 5
Q9CWV5 PRELIMINARY; PRT; 500 AA.
AC Q9CWV5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone-2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
GN Name=Plxcl1; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
ARAkawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
HANAGaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

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RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Segabe Y., Suzuki H., Tagami M., Tagawa A., Takabaishi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK010361; BAB26881.1; -.
DR MGD; MGI:1919574; Plxcl1.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004872; P.receptor activity; IEA.
DR GO; GO:0007275; P.development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CAl8BD CRC64;

Query Match 89.8%; Score 528; DB 2; Length 500;
Best Local Similarity 91.5%; Pred. No. 2.4e-47;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGCGTIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 60
    |||||
Db 138 LSPDFPPYGHPLRQITATGCGTIFMGDVHHRMLTATQYVAPLMAFNPGYSDNSTVVYFD 197
    |||||

Qy 61 NGTVFVVQWDHVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
    |||||
Db 198 NGTVFVVQWDHVYVQWEDKGSFTFQAALHHDGRIVFAYKEIPMAV 243
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RESULT 6
Q91ZV7 PRELIMINARY; PRT; 500 AA.
AC Q91ZV7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor endothelial marker 7 precursor.
GN Name=Plxcl1; Synonyms=Tem7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21433268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378760; AAL11997.1; -.
DR MGD; MGI:1919574; Plxcl1.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004872; P.receptor activity; IEA.
DR GO; GO:0007275; P.development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 500 AA; 55693 MW; 14FE25512A319DAF CRC64;

Query Match 89.8%; Score 528; DB 2; Length 500;
Best Local Similarity 91.5%; Pred. No. 2.4e-47;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 LSFDFPFYGHPLRQITTIATGTFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 60
Db 138 LSFDFPFYGHPLRQITTIATGTFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 197
Qy 61 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFYKEIPMSV 106
Db 198 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFYKEIPMAV 243

RESULT 7
Q8BM20
ID Q8BM20 PRELIMINARY; PRT; 507 AA.
AC Q8BM20;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER 7
DE homolog.
GN Name=Plxdcl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20493174; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK036144; BAC29318.1; -.
DR MGD; MGI:1919574; Plxdcl.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;

Query Match 89.8%; Score 528; DB 2; Length 507;
Best Local Similarity 91.5%; Pred. No. 2.4e-47;
Matches 97; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LSFDFPFYGHPLRQITTIATGTFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 60
Db 145 LSFDFPFYGHPLRQITTIATGTFPMGDVHRLMTATQVAPLMAFNPGYSDNSTVYVFD 204
Qy 61 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFYKEIPMSV 106
Db 205 NGTVFVQWHDVYVQWEDKGSFTFQAALHHDGRIVFYKEIPMAV 250

RESULT 8
Q96B59 PRELIMINARY; PRT; 480 AA.
AC Q96B59;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PLXDC2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012885; AAH12885.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;

Query Match 70.9%; Score 417; DB 2; Length 480;
Best Local Similarity 72.2%; Pred. No. 1.5e-35;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGSDNSTVYFD 60
Dy 112 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGSDNSTVYFD 171
Qy 61 NGTVFVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 108
Dy 172 NGTALVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 219

RESULT 9
Q6UX71 PRELIMINARY; PRT; 529 AA.
AC Q6UX71;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE ARFP2514.
GN ORFNames=UNQ2514;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Ligo D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358486; AAQ88850.1; -.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;

Query Match 70.9%; Score 417; DB 2; Length 529;
Best Local Similarity 72.2%; Pred. No. 1.5e-35;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGSDNSTVYFD 60
Dy 161 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGSDNSTVYFD 220
Qy 61 NGTVFVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVMSVPE 108
Dy 112 NGTALVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVMSVPE 220

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Db 221 NGTALVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268

RESULT 10
Q96PD9 PRELIMINARY; PRT; 529 AA.
AC Q96PD9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN Name=TEM7R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378757; AAL11994.1; -.
DR GenBank; HGNC:21013; PLXDC2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
DR Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 529 tumor endothelial marker 7-related.
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;

Query Match 70.9%; Score 417; DB 2; Length 529;
Best Local Similarity 72.2%; Pred. No. 1.5e-35;
Matches 78; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGSDNSTVYFD 60
Dy 161 LSPDFPPYGHPLRQITATGTFIFMGDVHRLMTATQYVAPLMANFNGSDNSTVYFD 220
Qy 61 NGTVFVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVMSVPE 108
Dy 221 NGTALVQWQDHVHLQDNVNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268

RESULT 11
AAQ88850 PRELIMINARY; PRT; 529 AA.
ID AAQ88850;
AC AAQ88850;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ARFP2514.
GN UNQ2514.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Ligo D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

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Db 161 LSPDFPPYGHFLNEVTATGGFIVTGEVHRMLTATQYIAPLMAFDPDSVSRNSTVRYFD 220
Qy 61 NGTVFVQWDRVYLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 221 NGTALVVQWDHVLQDNYNLGSFTFQATLLMDGRIFGYKEIPVLVTQ 268

RESULT 14
QD9C11 ID QD9C11 PRELIMINARY; PRT; 530 AA.
AC QD9C11; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
DE homolog.
GN Name=Plxdc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=92279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
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RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda S., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004640; BAR23431.1; -
DR MGD; MGI:1914698; Plxdc2.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR008947; PLCNuclease.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 530 AA; 59616 MW; FB956C020735E36D CRC64;

Query Match 69.9%; Score 411; DB 2; Length 530;
Best Local Similarity 70.4%; Pred. No. 6.4e-35;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 LSPDFPPYGHFLRQITATGGFIFMGDVHRLTATQYIAPLMAFDPDSVSRNSTVRYFD 60
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Db 161 LSPDFPPYGHFLNEVTATGGFIVTGEVHRMLTATQYIAPLMAFDPDSVSRNSTVRYFD 220

Qy 61 NGTVFVQWDRVYLQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 221 NGTALVVQWDHVLQDNYNLGSFTFQATLLMDGRIFGYKEIPVLVTQ 268

RESULT 15
QD9C11 ID QD9C11 PRELIMINARY; PRT; 530 AA.
AC QD9C11; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN Name=Plxdc2; Synonyms=fem7R;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378761; AAL1998.1; -
DR MGD; MGI:1914698; Plxdc2.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00423; PSI; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 30 Potential.
SQ SEQUENCE 530 AA; 59625 MW; FF8315020735E36D CRC64;

Query Match 69.9%; Score 411; DB 2; Length 530;
Best Local Similarity 70.4%; Pred. No. 6.4e-35;
Matches 76; Conservative 13; Mismatches 19; Indels 0; Gaps 0;
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Qy	1	LSRDPFPYGHPLROITTIATGGFIEMGDVIHMLTATQVAPLMANENPGYSDNSTVVYFD	60
Db	161	LSRDPFPYGHPLNEVTATGGFIYIGEVVHRMLTATQIIAPLMAFDFSVSRNSTVRYFD	220
Qy	61	NGTVFVVQWDHYYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE	108
Db	221	NGTALVVQWDHVLQDNVNLGSGFTFQATLLMDGRIIFGYKEIPVLVTQ	268

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Job time : 41.7978 secs